

**FIGURE 1**

CGGACGCGTGGGTGCGAGGCCAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTTAGA  
CCTGGTGCACCACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG  
GTTTTCCACCCAGCTTTTACCAAGGCCTCCCCTGTTGTGAAGAATTCATCACGAAGAATCA  
ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAACAAGAATTGGGATCCGGCGTGGGA  
GAACTGGCCAAGAACTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAAATATTTAAAATT  
GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA  
CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT  
ATGTCAAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT  
TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG  
GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC  
CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT  
GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC  
AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAGAAAGTTTCTGA  
ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG  
TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT  
AGTTCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT  
CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT  
ACATTAAATATATTTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**AG**  
**A**AGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAATGGGGCAGATATGC  
ATTAAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA  
TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT  
AATCCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT  
TTGGTGAATGTGAAAACATAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA  
TTTAGTAGGTTCACTGAGTAACATAAATTTAGCAAACCTGTGTTTGCATATTTTTTTGGAGT  
GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG  
GAGTCACCTGCAGTCTTTTGTTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA  
GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACAAGTGGTCATTGTTACATTCATTT  
GCTGAACTTAACAAAACCTGTTTCATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG  
CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC  
ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA  
ATAACTTTAAACATATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG  
AATACAAACAGTATACTCATG

**FIGURE 2**

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL  
KEAALEPSMEKIFKIDQMGRWFWAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI  
HSTMYLAGSIGLTALSAIAISRTPVLMNFMMRGWSWVTIGVTFAMVGAGMLVRSIPYDQSP  
GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL  
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMFLLYDTQKVIKRAEVSPMYGV  
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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**FIGURE 3**

GAAGGCTGCCTCGCTGGTCCGAATTCCGGTGGCGCCACGTCCGCCCGTCTCCGCCTTCTGCAT  
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCCGGCCGCGTCTGAGGG  
 GGTCCGCACGGGGAGTCGGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTCTGAAG**ATG**TCGG  
 ACATCGGAGACTGGTTTCAGGAGCATCCCGGCGATCACGCGCTATTGGTTCCGCCGCCACCGTC  
 GCCGTGCCCTTGGTCGGCAAACCTCGGCCTCATCAGCCCGGCCCTACCTCTTCTCTGGCCCCGA  
 AGCCTTCCCTTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG  
 GTCCAGGAACCTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGCGA  
 CTTGAAACAGGAGCTTTTGTATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTAACTG  
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA  
 TGTCAGTACTTTATGTCTGGGCCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA  
 ACACGATTTAAGGCCTGCTATTTACCCTGGGTATCCTTGGATTCAACTATATCATCGGAGG  
 CTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTCTTAATGTTCA  
 GATACCCAATGGACTTGGGAGGAAGAAATTTTCTATCCACACCTCAGTTTTTGTACCGCTGG  
 CTGCCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC  
 TGCTGATCAGAATGGCGGAGGGCGGGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC  
 AG**TGA**AGGGGGCGGCCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCTCCAGTGCTGGGTG  
 CACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTT  
 AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCCACAAGTTTACGAT  
 TCTCATTCAAGTCCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAATTGCAAACTGAC  
 TACATTTTTTGGTGTCTTCTCTTCTCCCTTTCCGTCTGAATAATGGGTTTTAGCGGGTCTT  
 AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAACCTTCCCAAAGGACCTTATCTCTT  
 TCTTGCACACATGCCTCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG  
 CCCATAAAATTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGGCAAGGCTGGTC  
 ACAACAATCATATTCACGTTATTTTCCCTTTTGGTGGCAGAAGTGTACCAATAGGGGGAG  
 AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATTGCTTCGACTGACATCCGTTGTT  
 AACCGTTTGGCACTCTTCAGATATTTTTTATAAAAAAGTACCACTGAGTTCATGAGGGCCA  
 CAGATTGGTTATTAATGAGATACGAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT  
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTAGGTTTAAACCATGGGGGATGCACCCC  
 TTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTGGCTTTGTGT  
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTGGAGAGGTCCTGGGCATTG  
 ATTCCCATTTCAATCTCATTTCTGGATATGTGTTTATTGAGTAAAGGAGGAGAGACCTCATA  
 CGCTATTTAAATGTCACTTTTTTGCCTATCCCCCGTTTTTTGGTTCATGTTTCAATTAATTGT  
 GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA  
 AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGGGTGTGTTA  
 TTTTGGTTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTT  
 TCGTAGGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAAATAAAGTTTTTTGAAGGCCA  
 TGGCTTTTACACAGTTATTTTATTTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT  
 ATTGAGTGGCTGTCACACTTTGAGGCAACTAAAAAGGCTTCAAACGTTTTTGATCAGTTTCTT  
 TTCAGGAAACATTGTGCTCTAACAGTATGACTATTCTTTCCCCACTCTTAAACAGTGTGAT  
 GTGTGTTATCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTTGTGTG  
 TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTCA  
 TGTTTTGTTGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAAATTTTAGAGGCCATTACT  
 CCAATTATGTTGCACGTACACTCATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATA  
 TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCCTCTTACCAGTCAGCTGCCTGCGAG  
 CAGTCATTTTTTCTAAAGGTTTACAAGTATTTAGAACTTTTCAGTTCAGGGCAAAATGTTT  
 ATGAAGTTATTCCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGATT  
 ATGTTTCTGGAATAATTTTACCAAACAAGCTATTTGAGTTTGGACTTGACAAGGCAAAACA  
 TGACAGTGGATTCTCTTTACAAATGGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCC  
 TTTTGTAAACTAATCCTTTTTTATTGGTAAAAATTGTAAATTAAATGTGCAACTTG

**FIGURE 4**

MSDIGDWFRSIPAITRYWFAATVAVPLVGLGLISPAYLFLWPEAFLYRFQIWRPITATFYF  
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP  
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL  
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL  
GDQ

**Transmembrane domain:**

amino acids 98-116, 152-172

**N-myristoylation site.**

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

**Glycosaminoglycan attachment site.**

amino acids 218-222



**FIGURE 5**

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG  
GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT  
CCTTGTGGCCCAAAGGCCTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTTGCC  
CCTTTGGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG  
CGGGGTTCCCTGCGAGGCCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT  
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT  
GGCCTGTGTTCCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC  
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT  
AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC  
CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA  
AAAACATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTACCT  
GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT  
GAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA  
AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG  
AATAATCCCAAGGGGATGGTGAACATTTTGCACACCCACCCTCAGAAGTTAAATGCATTT  
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAACTTCCTCCCTCC  
CACAAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC  
TTATCAGTACTTGAACAGAAGAAGCTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA  
TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG  
GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG  
CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**  
**A**TAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC  
CTTACACTG

**FIGURE 6**

MAAEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP  
LVFDDEEESKLTYTEIHQEYKELVEKLLLEGYLKEIGINEDQFQEAactsPLAKTHTSQAILQP  
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGLVLPDCLTDGSDVVSdleHEEMKILREVL  
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS  
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPiANLSVLGTEELRQREHYLKQKRDKLMS  
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRLLAEKLKEEVINK

**N-glycosylation sites.**

amino acids 224-228, 246-250, 285-289

**N-myristoylation site.**

amino acids 273-279

**Amidation site.**

amino acids 252-256

**Cytosolic fatty-acid binding proteins.**

amino acids 78-108

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**FIGURE 7**

GGGCACAGCACATGTGAAGTTTTTGGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT  
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA  
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG  
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC  
AGAAAAACATTGAAATGCAGCTGCAAGCCATTCTGAATAATTCAAGAGAGAAATGGTGTATTA  
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT  
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

**FIGURE 8**

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG  
 TAGCTTCTCCACGTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG  
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAAC  
 AGTGGAATGAAAAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC  
 ATTCCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT  
 CTGCCAATGAAGAAAAACAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTG  
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCAATCTGTGTTATAAAGAAAGATCATCAAAGTAG  
 AAATTTGAAATATGCTTCCTGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATTCTGCCT  
 TTCTTTATTTCTGGAATACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATG  
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCCAGGATAGTGCTGAA  
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT  
 TGACTGCCGGGACTAAAACTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC  
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAAGTGAAGTGTCCAGAAAAGACAATTG  
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTC  
 ACATCCGTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTTCTTCAATGGCT  
 AATATCTATAATGAAAAGATACTGAAGGAGGGGAACCAGCTCACTGAAAGCATCTTCATACA  
 GAACAGCAAACCTCTATTTCTTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCCTTCAGAGGA  
 GTAACCGTGATCAGATTAAGAACTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC  
 CTTATTTTTGTAACCTGCATTCAGGGCCCTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA  
 CATGTTCCATGTCTTGATGGCCCAGGTTACCACTGTCATTATCACAAACAGTGTCTGTCTCTGG  
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGGAAGCCCCATCAGTCCTTCTCTCTATA  
 TTTATTTTATAATGCCAGCAAGCCTCAAGTTCGGAATACGCACCTAGGCAAGAAAGGATCCG  
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA  
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA  
 GCTCTCTTGAACCTTATTTTTCACATTTTTCAGTGTTTGTAAATATTTATCTTTTCACTTTGATA  
 AACCAGAAATGTTTCTAAATCCTAATATTCTTTGCATATATCTAGCTACTCCCTAAATGGTT  
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCTAAAGAACTGATACAGGAGTAACA  
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT  
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTTGTAAATATCATGTTAGCTATAGCTTGTATAT  
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT  
 CTTCCCTTTTTTAACATTATAAAAGCTAGGTTGTCTCTTGAATTTTGAGGCCCTAGAGATAGT  
 CATTTTGCAGTAAAGAGCAACGGGACCCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC  
 CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAAATATTTTGCTGAAGAAGCAGT  
 TTCTCAGACACAACATCTCAGAAATTTAATTTTTAGAAATTCATGGGAAATTGGATTTTTGT  
 AATAATCTTTTGATGTTTTAAACATTGGTTCCTAGTCACCATAGTTACCACTTGTATTTTA  
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT  
 GTCATTACTCCTGAATTATTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACT  
 AATTCAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC  
 CAGATTGTCAGTGAAGCTGATGCCTAGGAACCTTTTAAAGGGATCCTTTCAAAAGGATCACTT  
 AGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAAGACC  
 AGTAATATATAAGTCACTTTACAGTGCTACTTTCACACTTAAAAGTGCATGGTATTTTTTCATG  
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA  
 AAATTAGCAAACAAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG  
 CTTTAACTGGCAGGCCTGTATGTTTACAGACTACCATACTGTAAATATGAGCTTTATGGTGT  
 CATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA  
 AGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAATTG  
 GTGGAAATTTGTAATTAATAATATTATTAACCT

**FIGURE 9**

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK  
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPMAMAV  
IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF  
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI  
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI  
FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI  
YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESDETF

**Transmembrane domains:**

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,  
298-318, 328-368

**N-glycosylation sites.**

amino acids 128-132, 204-208, 218-222, 374-378

**Glycosaminoglycan attachment site.**

amino acids 402-406

**N-myristoylation sites.**

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

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**FIGURE 10**

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG  
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC  
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG  
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGGAATGGAA  
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG  
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG  
AAAACAAGTATGATTATCTTCCAACACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT  
TTCTGTGTGCTTGTGTCAATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA  
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC  
TGGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTC  
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAGGATAGTGCTGAAGAGGCGTCTAAA  
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTGTCTATTGTGGCCTTGACTGCCGGGA  
CTAAAACTTTA

**FIGURE 11**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGGCGGCC  
GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCTGCGGGGCAGAGGAGCAT  
CCCGTCTACCAGGTCCCAAGCGGCGTGGCCCGCGGGTCATGGCCAAAGGAGAAGGCGCCGAG  
AGCGGCTCCGCGGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCCCCGGCCCA  
GGTGAAGAAAGAACCGAAAAAGAAGAAACAACAGTTGTCTGTTTGCAACAAGCTTTGCTATG  
CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC  
CTATTGG**ATG**TGGCTCAGGTGGGCCCTTTCTCTGCCTCCATCATCCTGTTTGTGGGCCGAGC  
CTGGGATGCCATCACAGACCCCTGGTGGGCCTCTGCATCAGCAAATCCCCCTGGACCTGCC  
TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCCCTGGCCGTCATTGCCTACTTCCTC  
ATCTGGTTCGTGCCCCACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT  
CTTTGAAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA  
ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC  
AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCTTGTTTCCAGG  
ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATAACATGGCACCCTTCACAC  
AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTG  
TGCTGTCTATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTG  
AGCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATAACATCAAACCTT  
ATTACTGGCTTCCTCTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTT  
TTGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCT  
CGGCCACTTTAACCATTCCCCTCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT  
GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA  
CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC  
TACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT  
GGAACCGAGCCCATCTTCTTCTCCTTCTATGTCTTCTTCACCAAGTTTGCCCTCTGGAGTGTG  
ACTGGGCATTTCTACCCTCAGTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC  
CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG  
CTGGGCCTGCTGCTCTTCAAATGTACCCCATTTGATGAGGAGAGGCGGCGGCAGAATAAGAA  
GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG  
AGCTGGCTAGCATCCTCT**TAG**GGGCCCGCCACGTTGCCCCGAAGCCACCATGCAGAAGGCCACAG  
AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA  
CTGAAGACTCAAGGAGGTGGCCCAGGACACTTGCTGTGCTCACTGTGGGGCCGGCTGCTCTG  
TGGCCTCCTGCCTCCCCTCTGCCTGCCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA  
TGCCAAGGACTGATCGGGCCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC  
TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTGTATGTATATGTCTGTGAGCTA  
TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

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**FIGURE 12**

MWLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG  
SCPTSHARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL  
GTAIQQQIVGQADTPCFQDFNSSTVASQSANTHGTTSHRETQKAYLLAAGVIVCIYIICAV  
ILILGVREQREPYEAAQQSEPIAYFRGLRLVMSHGPIYIKLITGFLFTSLAFMLVEGNFVLFCT  
YTLGFRNEFQNLALLAIMLSATLTPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI  
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG  
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL  
QALRDEASSSGCSETDSTELASIL

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**FIGURE 13**

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT  
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA  
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA  
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT  
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC  
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG  
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC  
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT  
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG  
GAACCGAGCCCAT

**FIGURE 14**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT  
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGCT  
GGTGGTTTTAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT  
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT  
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG  
CAGTTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA  
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTACTGAGTTGTTTAGG  
ACTTTCTATTGTGGCAAACCTTCAGAAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTG  
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG  
CAGCCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG  
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG  
ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT  
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA  
TTTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCCTCTATGACACTG  
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTGATGAAAGGAT  
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA  
TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA  
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA  
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

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**FIGURE 15**

MWWFQQGLSFLPSALVIWTSAAFI FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI  
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG  
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG  
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYD  
TAPCPINNERTRLLSRDI

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**FIGURE 16**

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT  
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA  
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGGAAGCAGT  
TACCAAGAATCTTCAACCCTTTCCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA  
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA  
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT  
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT  
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

**FIGURE 17**

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG  
CCGGGGTGCGGAGCCGAC**ATG**CGCCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC  
CTTCGCCTTGTACTTGCTGTGACGCGACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGG  
AGGCTGGAGGCAGGTCGCTGTGGTTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG  
GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTTGCTCTTCTGCGGCGCCTA  
CCTCTACAAACAGGGCTTTGCCATCCCCGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT  
TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC  
TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT  
GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT  
TGAGACTTTTCCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCCAATTCTGAACATT  
CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTATCTGTGT  
GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG  
TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCTCATTAAAAAATTT  
AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA  
CACAT**TGA**TCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA  
TGTGGTCCCTCTAAAGCCCCTCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG  
CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT  
TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT  
GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC  
ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAT  
ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGC  
AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT  
CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

**FIGURE 18**

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYR  
KEHQAYVFLLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS  
IFGKQLVVSYPDKVALLQRKVEENRNSLFFFLFLRLFPMTFNWFLNLSAPILNIPIVQFF  
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ  
LNETSTANHIHSRKDT

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 101-123, 189-211

**N-glycosylation sites.**

amino acids 172-176, 250-254

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 240-244, 261-265

**N-myristoylation site.**

amino acids 13-19, 104-110, 115-121, 204-210

**Amidation site.**

amino acids 27-31

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 4-15

**Protein splicing proteins.**

amino acids 25-31

**Sugar transport proteins.**

amino acids 162-172

**FIGURE 19**

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT  
CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAA  
TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA  
TTTATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG  
TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC  
CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT  
TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT  
GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA  
GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC  
CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC  
AACTGCACTGGCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA  
ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCCTGTTGGAGGAAGAGATTC  
AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG  
TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA  
CAGATCACAAATGTTACGTGAGCTTTTTCTGTCTTCACTCACCTGCCATTTCCAAAAGATG  
CCTCTTTAAACAAGTGCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG  
ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA  
GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG  
ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT  
GGAACCGCTTTCTCAGAACTGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA  
AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAAA

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## **FIGURE 20**

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVY  
KVLATLGLILLTAYFVIQPFSPPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL  
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT  
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELPV  
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRHRCQSVAMP  
IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

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**FIGURE 21**

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG  
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTTCAGTTGTGATC  
AAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT  
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTCAGAGACTGTTG  
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC  
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT  
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC  
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

CCACACGCGTCCGCCCAACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG  
CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG  
CCACTGGTGCACGCTGCTAGACCGTGCTATGAGCCGCTGGGGCTGCAGTGGGGACTGCC  
CTCCCTGCCACCCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA  
CACCCGAATGGCGCCACTTTCATGCACAAACAGGTACAGCCAACTGCTCCAGTTCGAAATG  
GACACGTATGCTAAGAGCCACGACCTATGTGAGGTTTCTGGAATGCCTGCTATGACATGCT  
TATGAGCAGTGGGCAGCGGCGCCAGTGGGAGCGCGCCAGAGTCGTCGGGCCTTCCAGGAGC  
TGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCCTGGAGGGGCTACGCTACACGGCAGTGCTG  
AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCAGTGGGGGGCGCTGTGGCGCCAGCT  
CGCCAGCCCATGTGGGGCCTGGGCGCTGAGGGACACTCCATCCCCCGCTGGAACACTGTCC  
GCGCCGAGACATATTACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCCTAC  
CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCCCTGACACCCACCGAGGAGGC  
TCACTGCCTCTGGCAGTGACCAAAGAGGGCCAAAGTGAGCACCCACCCGAGTTGCTGCAGG  
AGGACCAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCCGATGGAGGCAGCAGAAGCTG  
GATGAGCAGCGTGAGAAGCTGGTGCTGTCGGCCGAGTGCCAGCTGGTGACGGTAGTGCCGTG  
GGTCCCAGGGCTGCTGGAGGTCACCAACAGAAATGTATACTTACGATGGCAGCACTGAGC  
GCGTGGAACCGAGGAGGGCATCGGCTATGATTTCCGGCGCCCATGGGCCAGCTGCGTGAG  
GTCCACCTGCGGCGTTTCAACCTGCGCCGTTACGCACTTGAGCTCTTCTTTATCGATCAGGC  
CAACTACTTCCCTCAACTTCCCATGCAAGGTGGGCACGACCCAGTCTCATCTCCTAGCCAGA  
CTCCGAGACCCAGCCTGGCCCCATCCCACCCCATACCCAGGTACGGAAACCGGTGATACTCG  
TGGTCTCTGCGCTACCGGCCCCCTCTCAAGCTACCTAAGCAGCCGCTCCCCAGGAGAT  
GCTGCGTGCCCTCAGGCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTTCGAGTACT  
TGATGCAACTCAACACCATTGCGGGGCGGACCTACAATGACCTGTCTCAGTACCCTGTGTTT  
CCCTGGGTCTGTCAGGACTACGTGTCCCCAACCCCTGGACCTCAGCAACCCAGCCGTCTTCCG  
GGACCTGTCTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAGAAGT  
ATGAAAGCTTTGAGGACCCAGGAGGACCATTGACAGGTTCCACTATGGCACCACACTCC  
AATGCAGCAGGCGTGATGCACTACCTCATCCGCGTGGAGCCCTTCACCTCCCTGCACGTCCA  
GCTGCAAAGTGCGCCGCTTTGACTGCTCCGACCGGCAGTTCCACTCGGTGGCGGCAGCCTGGC  
AGGCACGCCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTCTTCTACTTTCTT  
GACTTCTCTGGAGAACCAAGACGAGTTTGAACCTGGGCTGTCTCCAGCTGACCAACGAGAAGT  
AGCGCATGTGGTGCTACCCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCAGCCGC  
AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC  
TACAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA  
GGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGGCATTA  
TCAAGCAACTTTGGGCAGACTCCCTGTGAGCTGCTGAAGGAGCCACATCCAACCTCGGCTCTCA  
GCTGAGGAAGCAGCCCATCGCTTGCACGCCTGGACACTAAGTACCTACCTAGCATCTCCAGCA  
CCTGGACGAACCTCAAGGCATTCTTTCGACAGAGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA  
CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAGACCCC  
ACCATGGGCAGCCACAAGACGCAGCGCACTGCTGAGTGGCCCGTGGGTGCCAGGCAGTGGTGT  
GAGTGGACAAGCACTGGCAGTGCGCCCCGGATGGAAGCTGCTATTACGCGTGGCCACTGGG  
ATGGCAGCCTGCGGGTGACTGCATAACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC  
CTTGATGTAGTAACCTGCCTTGCAGTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG  
GGACACCACGTGCATGGTGTGGCGGCTCCTGCATCAGGCTGGTCTGTGAGTAGGCCTGGCAC  
CAAAGCCTGTGACAGGTCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT  
GAACCTGACATGGCTGTGTCTGGATCTGAGGATGGAACACTGTATCATACACACTGACGCCG  
CGGACAGTTTGTAGCGGCACTACGGCTCTGGGTGCCACATTCCCTGGACCTATTTTCCACC  
TGGCATTTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACGTCTTGGGGCC  
CAGGTACCTACTCCTTGCACCTGTATTAGTCAATGGGAAGTTGCGGGCTTCACTGCCCT  
GGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTGTGTGTGCTGGGCACCGCCAGT  
GCGCCCTGCACATCTCCAACATAACACACTGCTCCCGCCCGCCTCCTTGGCCCATGAAG  
GTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCAGCCAGCTGCTGGTGGGCTGGAGGA  
TGGCAAGCTCATCGTGGTGGTGCAGGGGCGGCCCTCTGAGGTGCGCAGCAGCCAGTTTCGCGC  
GGAAGCTGTGGCGGTCTCTCGCGGCGCATCTCCAGGTGTCTCGGGAGAGACGGAATACAAC  
CCTACTGAGGCGCGCTTGAACCTGGCCAGTCCGGCTGCTCGGGCCCCCGCCCCCGGCGAGGCTG  
GCCCGGGAGGGCCCCGCCAGAAGTCGGCGGGAACACCCCGGGTGGCGAGCCAGGGGGTGA  
GCGGGGCCACCCCTGCCAGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG  
GGCGGAAGTCCCGCCCCCTCGCCGGCTGAGGGGGCGGCCCTGAGGGCCAGCACTGGCGTCT

**FIGURE 23**

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL  
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN  
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELTP  
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP  
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTVPSSPSQTPRPQPGPIPPHTQV  
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRITYNDL  
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKEYESFEDPAGTIDKFH  
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADVKEIIP  
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQQHRQALESEYVSAHLHEW  
 IDLIFGYKQGRGPAEEALNVFYYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP  
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF  
 SFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVTALPRGKLL  
 SQLSCHLDVVTCLALDTCGIYLIISGSRDTTCMVWRLHQQGLSVGLAPKPVQVLYGHGAAS  
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSA  
 WERPGAQVTYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA  
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSS  
 GETEYNPTAR

**N-glycosylation site.**

amino acids 677-681

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 985-989

**Tyrosine kinase phosphorylation site.**

amino acids 56-65, 367-376, 543-551

**N-myristoylation site.**

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,  
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,  
 873-879, 912-918, 954-960

**FIGURE 24**

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC  
CACGGCCCACCTTGTGAACTCCTCGTGCCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT  
CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCCTGGGGCTCTTC  
TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCCCTCGCTGGAGCCTTTGCCTCCTT  
CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC  
GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG  
ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC  
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC  
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA  
AATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGTCGTCCTGGACAAAGTCACAGA  
CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTGGAGGCGTGGGGGTCTGTCTTCTTTT  
TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCCACCTCAACTATTAC  
TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTCAGCGT  
TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG  
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC  
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGGCCCTGATCCAGGACTGC  
ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT  
AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG  
AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC  
GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTAC  
TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA  
TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA  
AAAGATTTTATTAAAGATATTTTGTAACTC

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**FIGURE 25**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVVLGLF  
WTLNWWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ  
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK  
NAFMLLMRNIVRVVLDKVTDLLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYY  
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKK  
EAPPDNKKRKK

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**FIGURE 26**

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGT  
GGCT**ATG**TTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC  
TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT  
CAGTGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC  
ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG  
ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG  
CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA  
TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT  
CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA  
GTGGAGCAAACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT  
CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG  
CTTGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC  
CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG  
CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA  
CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC  
AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA  
GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCCTGAAGCAGGTGAAGCAGAAGTTCC  
AGGCCATGGACATCTCCTTGAAAGGAGAAATTTGCGGGAAATGATTGAAGAGTCTGCAAATAAA  
TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAGCACAAAGTT  
TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT  
CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG  
TACCATGGCCTGGAACCTGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC  
CTTTGCACCAACCTCGTCATCTCCCAGGGGCCTTTCCTGTACTGCTCTCTCATGGAGGGCAC  
TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA  
AGTCCTTTGTGTGTTTCGACAAAGAACCGGCGCTGCAAACCTGCTGCCCCTGGTGATGGCTGCC  
CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC  
GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA  
TGCTGCACAACCATTTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT  
CTGGACGCACTTATTTCCCTCCTGTCC**TAG**GAATTTGATTCTTCCAGAATGACCTTCTTATT  
TATGTAACCTGGCTTTCATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT  
TTTTATTAAATAAAATGCTTATTTTAGGAAA

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## **FIGURE 27**

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF  
LEHKEQFHYFILINCGANVDLLDILQPEDDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD  
LEVPAIEDIFRDEEEDDEHSGNDSGSEPSEKRTRLEEEIVEQTMRRRQRREWEARRRDILF  
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRH  
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR  
LQEF LADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL  
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL  
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP  
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL  
DALISLLS

**FIGURE 28**

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA  
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT  
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT  
GGTTCAGTTTCTGGGTGGCAAGAAGTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC  
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT  
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA  
CGATACCC



**FIGURE 29**

CAGGAACCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTTCTAGTGAAC  
 CACGAAGGGACGATACCAGAAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG  
 GCTGACTTTGGCTATAGAAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGGAAAGCTAA  
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAACAATT  
 GAGTAAAGTACGCTCCGGTCACC**ATG**GTGACAGCCGCCCTGGGTCCCCTCTGGGCAGCGCTC  
 CTGCTCTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC  
 CAGCGGCTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAG  
 CCTCTTCTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTACATTAATATCACCATC  
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGG  
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG  
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC  
 GGCGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA  
 CATGGCGACCCGCCAGTTTGTGCTGCTCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGC  
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGGCTGTCTATC  
 CTGTACGCGCAGCCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC  
 CTACGGGGACCGCGTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCA  
 ACGACTTCGACACCTACATCACCTCAGCGGCCACCTCATCAAGGCCGAGGACGAC**TGAGGG**  
 CCTCTGGGCCACCCCTCCCGCTGGAGAGCTCAGGTGCTGGTCCCCTGCCCTGCAGGGCTCAG  
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGA  
 CCCTGCTTCTATCTTGGCTGCCATCATCCCTCCAGCCTATTTCTGCTCCTCTCTCTCTCT  
 TGGACCTATTTAAGAAGCTTGCTAACCTAAATATTCTAGAACTTTCCAGCCTCGTAGCCC  
 AGCACTTCTCAAATTTGAAATGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCT  
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTG  
 ATGGGGTCACTCTATGAACCACACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAG  
 TACTTTCTGAACATTCTGGAATCCTCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTTCT  
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGAATCTCAGTTCACTGC  
 AACCTTCGCTCCCGGGTTCAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC  
 AGGCGCTCTCCTACCATGCCTGGCTAATTTTGTATTTTGTAGTAGAGATGGGGTTTACCATA  
 TTGGCCAGGCTGGTCTTGAACCTCCTGACTTCAGGTGACCCACCCGCCCTCGGCCTCTCAAAT  
 GCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCCAATTCCAACATTCTTAAATTCTCTCAT  
 CCCTCCAGGGCTCCCCGTGCTATGTTCTCTTTACCCCTTCCCCCTCTTCTCTGCTCAGGCC  
 TGCACCACTGCAGCCACCGTTTCAATTTATTTCATTTCATTAAACACTGAGCACTCACTCTGTGCT  
 GGGTCCCGGGAAGGGTGAGGGGGTCAAGACACAGGCCCTGCCCTGCCCTCAGTGAAGTGGCCA  
 GTCCAGCCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCATGGGG  
 GCCTGTGTTCTGGGTGTTCAAGGTGCTGCTGGTCCCTCCATTACCCACTGCTCCCCAAGGCTGG  
 TGGGACGGGGTCCCGGTGGCAGGGGCAGGTATCTCCTTCCCGTTCCCTCATCCACCTGCCAG  
 TGCTCATCGTTACAGCAAACCCAGGGGGCCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG  
 ACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGCCCCGAAGAATGGAACCCACACCCA  
 TAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAGACCTGCCCTCCTCACTGGGATCCC  
 CTTCTGCTCCTCCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAAGTCATCT  
 GAACTTCCGTTTCCCCAGGGCCTCCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCT  
 CTCTGCCCCCTCATGCCCCCTCTCACCGGCCAGTGCCCCGACTCTCCAGGCTTTATCAAGGTG  
 CTAAGGCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCCTCCTCCGGCCTGGTGCTGCCTTTAC  
 AAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG  
 AGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCGTTTCTTCTCCAGGGTGGGGTGGCCTGGT  
 GTTCCCCTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAGAGGGAGGCGGCCCTCCGC  
 CCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGTGTCTCTGTGCTCAC  
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGCCAGGA  
 AGACCTGTGCTATAAACACCCTGCCTGATCCTGCCCTGCCTGACCCCGCCACGCCCTGCC  
 GTCCAGCATGATTAAAGAATGCTGTCTCCTCTTGAAAAA

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## **FIGURE 30**

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH  
ALPEIRPYINITILKGDGDPGPMGLPGYMGREGPQGEPGPQGSGDKGEMGSPGAPCQKRF  
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET  
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT  
FSGHLIKAEDD

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 72-75

#### **Clq domain proteins.**

amino acids 144-178, 78-111 and 84-117

**FIGURE 31**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCCGACCCGCCAGGAAAGACTG  
 AGGCCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCCGCCCTCCCGGGACAGAAG**ATG**TG  
 CTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAGG  
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCCGCCAGGGG  
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT  
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCCTGGACCTGTAC  
 AGAACCAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTG  
 GACCTGACGGCCAACAGGCTGCATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCT  
 CGAGCGCCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC  
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCCGCTGCGC  
 CTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCCGGCAT  
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG  
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAG  
 CGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACAC  
 CCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATG  
 TGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCGCCTGCGG  
 CTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTG  
 GGTGCGCGAGAGCCACGTCACTTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCA  
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCCAGCCACCACC  
 ACCACAGCCACAGTGCCCCACCACGAGGCCCGTGGTGCGGGAGCCCACAGCCTTGTCTTCTAG  
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCA  
 CTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC  
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTT  
 CACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTCA  
 CGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGC  
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA  
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG  
 AGTACACGGTCACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTGTCATGCCTTTGGGG  
 CCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTGCGGGGAGGGCCATACACCCCCAGCCGTCCA  
 CTCCAACCACGCCCCAGTCACCCAGGCCCGCGAGGGGCAACCTGCCGCTCCTCATTGCGCCCG  
 CCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGG  
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCT  
 GGAAGTGGAGGGAGTGAAGGTCCCTTGGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAG  
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTC  
 CAGTCACCCCTCCACGCAAAGCCCTACATC**TAA**GCCAGAGAGAGACAGGGCAGCTGGGGCCG  
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCC  
 CAACCTCGGGGATGTGTGACAGAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA  
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC  
 CGAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG  
 GGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA  
 CCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTG  
 TGAAGTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTA  
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG  
 GGAAGATGTTTTTCAAATCAGAGACAAGGACTTTGGTTTTTGTAAGACAAACGATGATATG  
 AAGGCCTTTTGTAAGAAAAAATAAAAGATGAAGTGTGAAA

**FIGURE 32**

MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDVPPDTVGLYVFEN  
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR  
RLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP  
GILTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAG  
NTRIAQLRPEDLAGLAALQELDVSNSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG  
PWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPTRPVVREPTALS  
SSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPE  
GFTGLYCESQMGQGTTPVTPRPPRSLTGLIEPVSPTSLRVGLQRYLQSSVQLRSLRL  
TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPA  
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQVGPGAG  
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPLHAKPYI

**FIGURE 33**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT  
 CTTTCATCATTCATATGAGGAAATAAGTGGTAAAAATCCTTGGAATAACA**AT**GAGACTCATCAG  
 AAACATTTACATATTTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG  
 AAGAAAGGGAAGTATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG  
 ACCCCAGGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTCAGA  
 TTTTCATTCTGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCACACAGCTGG  
 ATCTCAAAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTG  
 AAGAGTGTAACCTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTAATGACTT  
 TGACACCATGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTTGA  
 GTGGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTC  
 TTCTTAGGATTTCAGAACTCTTCCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAAC  
 AAAACTGCACATTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGGTGATGGAATCA  
 AGACTTCAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA  
 ATGCAACGAAATCTTAGTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA  
 TTTACTCTGGGACGACCTTTTCCTTATCTTACAATTTGTTGGCATAACATCAGTGGAACTACT  
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC  
 TCAAATACTGTAATGAGAACTATAAAATTTGGAGCATGTACATTTTCAGAGTGTTTTACATTCA  
 ACAGGATAAAAATCTATTTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAATG  
 CACAAATGCCACACATGCTTTTCCCGAATTATCCTACGAAATTCCAATATTTAAATTTTGCC  
 AATAATATCTTAACAGACGAGTTGTTTAAAAGAACTATCCAAGTGCCTCACTTGAAAACCTCT  
 CATTTTGAATGGCAATAAACTGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACAC  
 CCTTGGAACTCTGGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA  
 TGGCCAGAACTGTGGTCAATATGAATCTGTACATAATAAATTGTCTGATTCTGTCTTCAG  
 GTGCTTGCCCAAAAGTATTCAAATACTTGACCTAAATAATAACCAAATCCAACTGTACCTA  
 AAGAGACTATTCATCTGATGGCCTTACGAGAACTAAATATTGCATTTAATTTTCTAACTGAT  
 CTCCCTGGATGCAGTCATTTGAGTAGACTTTGAGTTCTGAACATTGAAATGAACCTTCATTCT  
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACTCTAAATGCGGGAAGAA  
 ATCCATTCCGGGTGTACCTGTGAATTAATAAATTTTCATTTCAGCTTGAAACATATTCAGAGGTC  
 ATGATGGTTGGATGGTCAGATTCATACACCTGTGAATACCTTTAAACCTAAGGGGAAGTAG  
 GTTAAAAGACGTTTCATCTCCACGAATTATCTTGCAACACAGCTCTGTTGATTGTCAACATTG  
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCCC  
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAACAACCCA  
 AGAACAACTCAAGAGAAATGTCCGATTCCACGCATTTATTTTCATACAGTGAACATGATTCTC  
 TGTGGGTGAAGAATGAATTGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTGTC  
 CTTTATGAAAGCTACTTTGACCCTGGCAAAAGCATTAGTGAAAATATTGTAAGCTTCATTGA  
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT  
 ATGAATTCTACTTTGCCCAACCAATCTCTCCATGAAAATTCTGATCATATAATTTCTTATC  
 TTACTGGAACCCATTCCATTCTATTGCATTCCCACCAGGTATCATAACTGAAAGCTCTCCT  
 GGAAAAAAAAGCATACTTGGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCAA  
 ACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCAGAGAAATGTATGAACCTGCAGACA  
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTGTCT  
 A**TAA**AATCCCACAGTCCCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTGATA  
 CAACCTTTATGATGGCAATTTGACAATATTTATTAAAAATAAAAAATGGTTATTCCTTCATA  
 TCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACACCTTCACAAGTTTATAAGG  
 GCTTATGGAAAAAGGTGTTTCATCCCAGGATTGTTTATAATCATGAAAATGTGGCCAGGTGC  
 AGTGGCTCACTCTTGTAAATCCCAGCACTATGGGAGGCCAAGGTGGGTGACCCACGAGGTCAA  
 GAGATGGAGACCATCCTGGCCAACATGGTGAAACCTGTCTCTACTAAAAATACAAAAATTA  
 GCTGGGCGTGATGGTGCACGCCTGTAGTCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCG  
 CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTGCACTCCAGCCTGGT  
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGGAAAAACATCC  
 TCATGGCCACAAAAAAGGTCTAATTCATAAATTATAGTACATTAATGTAATATAATATTA  
 CATGCCACTAAAGGAATAAGGTAGCTGTATATTTCTGGTATGGAAAAACATATTAATAT  
 GTTATAAACTATTAGGTTGGTGCAAACTAATTGTGGTTTTTGCCATTGAAATGGCATTGAA  
 ATAAAAGTGTAAGAAATCTATACCAGATGTAGTAACAGTGTTTGGGTCTGGGAGGTTGGA  
 TTACAGGGAGCATTTGATTTCTATGTTGTGTTTCTATAATGTTTGAATGTTTAGAATGA  
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

**FIGURE 34**

MRLIRNIYIFCSIIVMTAEGDAPELPEERELMTNCSNMRLKVPADLTPATTTLDLSYNLLFQ  
LQSSDFHSVSKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL  
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP  
ILNTTKLHIVLPMDTNFVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL  
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR  
VFYIQQDKIYLLLTCKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP  
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNDENCSPETVVNMNLSYNKLS  
DSVFRCLPKSIQILDNLNNNIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE  
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN  
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRV  
RKTQTQQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI  
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHNNLFHENS DHIILILLEPIPFYCIPTRYHK  
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM  
RTDCL

**FIGURE 35**

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACACCTGCCTCCAAGGACCGGCCTCGGAGGGGTGCGCGGGAAAGG  
 GAGGGAAGAAGGAAGGGCGGGGCGGGCCCCCTGCGCCCCCGCGCCTCTGCGCGCCCCGTCCGCCCCGGC  
 CCAGCCCAGCCCAGCCCCGCGGGCCGGTACACGCGCAGCCAGCCGGCCGCTCCCGCGCCAAGCGCGCCGT  
 CTGCTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCCCGAGCCCCGGCGCCCCGGTGACCGTGA  
 CCCTGCCCTGGGCGCGGGGCGGAGCAGGC**ATGT**CCCCCGGGGACCGCTACCCAGCGCTGGCCCTGGTGCTC  
 CTGGCAGTGACCTGGCCGGGGTTCGGAGCCCAGGGCGCAGCCCTCGAGGACCCTGATTATTACGGGCAGGAGAT  
 CTGGAGCCGGGAGCCCTACTACGCGCGCCCGGAGCCCGAGCTCGAGACCTTCTCTCCGCGCTGCCCTGCGGGGC  
 CCGGGGAGGAGTGGGAGCGGCGCCCCGAGGAGCCAGGCCGCCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCC  
 AAGAGGGAGAAGTCGGCTCCGGAGCCGCTCCACCAGGTAACACAGCAACAAAAAGTTATGAGAACCAAGAG  
 CTCTGAGAAGGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTGAGAGAGAGTTGCCACCTC  
 TTGGTCTGGAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCCTGGGGGCA  
 CATCGAGGGAGACTCAACATCCAGGCGGGCATTAAATGAAATGATTTTATGACGGAGCGTGGTGCGCGGGAAG  
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGGTGTCACTCAAGGGA  
 GGAACCTCCCTCTGGCTGAGTGACTGGGTGACATCCTATAAGGTCATGGTGAGCAATGACAGCCACAGTGGGT  
 ACTGTTAAGAATGGATCTGGAGACATGATATTTGAGGAAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCT  
 ACCCGTCCCCATGGTGGCCCGCTACATCCGCATAAACCCCTCAGTCTGGTTTGATAATGGGAGCATCTGCATGA  
 GAATGGAGATCCTGGGCTGCCACTGCCAGATCCTAATAATTATTATCACCGCCGGAACGAGATGACCACCACT  
 GATGACCTGGATTTTAAGCACCACAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCC  
 CAATATCACCAGAATTTACAACATTGGAAGAAAGCCACAGGGCCTGAAGCTGTATGCTGTGGAGATCTCAGATC  
 ACCCTGGGGAGCATGAAGTCGGTGAGCCCCGAGTTCACACTACATCGCGGGGGCCACGGCAATGAGGTGCTGGGC  
 CGGGAGCTGCTGCTGCTGCTGGTGCAGTTCGTGTGTCAGGAGTACTTGGCCCGGAATGCGCGCATCGTCCACCT  
 GGTGGAGGAGACGCGGATTACGTCCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCCTACGAAGGGGGCT  
 CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTCCCTGATTTA  
 AACACGCTGCTCTGGGAGGCAGAGGATCGACAGAATGTCCCCAGGAAAGTTCCCAATCACTATATTGCAATCCC  
 TGAGTGGTTTCTGTGCGAAAATGCCACGGTGGCTGCCGAGACCAGAGCAGTCATAGCCTGGATGGAAGAAATCC  
 CTTTTGTGCTGGGCGGCAACCTGCAGGGCGGGCAGCTGGTGGTGGCGTATCCCTACGACCTGGTGCGGTCCCCC  
 TGGAAGACGCAGGAACACACCCCCACCCCCGATGACCACGTGTTCCGCTGGCTGGCCTACTCCTATGCCTCCAC  
 ACACCGCCTCATGACAGACGCCCCGAGGAGGGTGTGCCACACGGAGGACTTCCAGAAGGAGGAGGGCACTGTCA  
 ATGGGGCCTCCTGGCACACCGTGCCTGGAAGTCTGAACGATTTAGCTACCTTCATACAACTGCTTCGAACCTG  
 TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCCGAGGAGTGGGAGAATAACCGGGAATC  
 TCTGATCGTGTTTCATGGAGCAGGTTTCATCGTGGCATTAAAGGCTGGTGAGAGATTACATGGAAAAGGAATCC  
 CAAACGCCATTATCTCGTAGAAGGCATTAAACCATGACATCCGAACAGCCAACGATGGGATTACTGGCGCCTC  
 CTGAACCCCTGGAGAGTATGTGGTCACAGCAAAGGCCGAAGGTTTCACTGCATCCACCAAGAACTGTATGGTTGG  
 CTATGACATGGGGGCCACAAGGTGTGACTTCACACTTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATGG  
 AGAAGTTTGGGAAGCAGCCCGTCAGCCTGCCAGCCAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACAGCGT  
 GGGTGA**CCCT**CCTGGGCCCTTGAGACTCGTCTGGGACCCATGCAAATTAAACCAACCTGGTAGTAGCTCCATAG  
 TGGACTCACTCACTGTTGTTTCTCTGTAATTCAAGAAGTGCCTGGAAGAGAGGGTGCATTGTGAGGCAGGTCC  
 CAAAAGGAAGGCTGGAGGCTGAGGCTGTTTTCTTTTCTTTGTTCCATTTATCCAAATAACTTGGACAGAGCA  
 GCAGAGAAAAGCTGATGGGAGTGAGAGAACTCAGCAAGCCAACCTGGGAATCAGAGAGAGAAGGAGAAGGAGGG  
 GAGCCTGTCCGTTAGAGCCTCTGGCTGCATAGAAAAGGATTCTGGTGCTTCCCTGTTTGGCTGGCAGCAAGG  
 GTTCCACGTGCATTTGCAATTTGCACAGCTAAAATTGCAGCATTTCCTCCAGCTGGGCTGTCCCAAATGTTACCA  
 TTTGAGATGCTCCCAGGCGTCTAAGAGAATCCACCCTCTCTGGCCCTGGGACATTGCAAGCTGCTACAAATAA  
 ATTCTGTGTTCTTTTGACAATAGCGTCATTGCCAAGTGCACATCAGTGAGCCTCTTGAATCTGTTTAGTCTCCT  
 TTTTCAACAAAGAGTGTGTTTCAGAAAAGGAGAGAGAGGCTGAGATCATTGAGGAGTTTGTGGGCGAGCAAGCA  
 TGGAGCTTCTTGACAAATTCTGGGTCCATAACAACCCCCAAAGTCCCTGCTGATCCAGTAGCCCTGGAGGTT  
 CCCCAGGTAGGGAGAGCCAGAGGTGCCAGCCTTCTGAAGGGCCAGAAAATTTAGCCTGGATCTCCTCTTTTAC  
 CTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCCTGAAGCCCTCTCTGCTTGAGGTATTGCCCTGTGTG  
 GAATTGAGTGCTCATGGGTTGGCCTCATATCAGCCTGGGAGTTATTTTGTATGTAGAATGCCAGATCTTCCA  
 GATTAGGCTAAATGTAATGAAAACCTCTTAGGATTATCTGTGGAGCATCAGTTTGGGAAGAATTATTGAATTAT  
 CTTGCAAGAAAAAGTATGTCTCACTTTTGTAAATGTGTGCGCTCATTTGACCTGGGAAAAATGAAAAAAA  
 AATAAAGCAAATGGTAAGACCCTTAAAAA

**FIGURE 36**

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLP  
AGPGEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS  
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA  
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF  
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT  
TDDLDKFHHNYKEMRQLMKVVMEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF  
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPBGYEKAYEGG  
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA  
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSAST  
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES  
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLL  
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR  
LKLGRGRRRQRG



**FIGURE 37**

CTAAGAGGACAAGATGAGGCCCGCCTCTCATTTCTCCTAGCCCTTCTGTTCTTCCTTGGCCAAGCTGCAGGGG  
ATTTGGGGGATGTGGGACCTCCAATTTCCAGCCCCGGCTTCAGCTCTTTCCAGGTGTTGACTCCAGCTCCAGC  
TTCAGCTCCAGCTCCAGGTGCGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTTCTGTGTCCCAGTTGTT  
TTCCAATTTACCCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACCACCTTTC  
CCGTGGACAGAGTGGAACGCTTGGAATTCACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAGAACTTTCTAAA  
GTGAGGGAATATGTCCAATTAATTAGTGTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATTGACATCAT  
GGAGAAGGATACCATTTCTTACACTGAACTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC  
TGGTCATACAGCTGAAGGAGAGTTTTGGTGGAAGCTCAGAAATTGTTGACCAGCTGGAGGTGGAGATAAGAAAT  
ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATGTCTTGCCATTGCGCCGAGAAATCGTGGC  
TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAAACACCCCTGTGCTCCACCCTCCTCCACTC  
CAGGGAGCTGTGGTTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGTGGTTTCAGCTCAACTGGAGAGGGTTT  
TCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCCAGCATCCAAACAAAGGACTGTATTGGGTGGCGCC  
ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTTGCTATTGTATATAA  
ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC  
ATGTACAACACCGGGAATATTGCCAGAGTTAACCTGACCACCAACACGATTGCTGTGACTCAAACCTCTCCCTAA  
TGCTGCCTATAATAACCGCTTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG  
GATTGTGGGTATTTTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACACTT  
CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCTTCATGGTATGTGGGGTTCT  
GTATGCCACCCGTACTATGAACACCAGAACAGAAGAGATTTTTTACTATTATGACACAAACACAGGGAAGAGG  
GCAAACCTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTTGACCAGAAA  
CTTTATGTCTATAACGATGGTTACCTTCTGAATTATGATCTTTCTGTCTTGCAGAAGCCCCAGTAAAGCTGTTTA  
GGAGTTAGGGTGAAAGAGAAAAATGTTTGTGAAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT  
CTAAAAGTGTGTTTCAATTTTGCAGCAATGTTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT  
TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGAATAAAGTCTGTCTAGGGTGGGA  
TTGTGAGAGGTCTAGGGGCACTGTGGGCCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA  
GGAATTAAGGAACCTTAAACTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAAATATTGCCCAATGACTAGTC  
CTCATCCATGTAGCACCCTAATTCTTCCATGCCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCT  
GGAGCTCCTCGAGGGACCAATCTCCAACCTTTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG  
CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAAGTGCTGAGTTTTATGGAGAGAGGCCCTTTTT  
ATGCATTAAATTGTACATGGCAAATAAATCCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTTCTTTCTCTC  
ATTGTCCACCTTACTAAAAGTCAGTAGAATCTTCTACCTCATAACTTCCTTCCAAGGCAGCTCAGAAGATTAG  
AACCAGACTTACTAACCAATTCACCCCCCACCACCCCTTCTACTGCCTACTTTAAAAAAATTAATAGTTTT  
CTATGGAAGTATCTAAGATTAGAAAAATTAATTTCTTTAATTTTATTATGGACTTTTTATTACATGACTCTA  
AGACTATAAGAAAATCTGATGGCAGTGACAAAGTGCTAGCATTTATTGTTATCTAATAAAGACCTTGGAGCATA  
TGTGCAACTTATGAGTGTATCAGTTGTTGCATGTAATTTTTGCCTTTGTTTAAGCCTGGAACCTGTAAGAAAAT  
GAAAATTTAATTTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT  
TGGAAACCTTGCTGGTGTATGTGATGTGCTTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT  
TCCTTTGATGTTCAAGTCCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCCCTTTTAAATAAATGAT  
TAAATGTGCTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 38**

MRPGLSFL LALLFFLGQAAGDLGDVGPPIPSPGFSSFP GVDSSSSSFSSSSSRSGSSSSRSLSGS  
GGSVSQ LFSNFTGSVDDRGT CQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV  
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ  
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKT KLKECEASKDQNTPVVHPPPTPGSCGH  
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYS PQHPNKGLYWVAPLNTDGRLL EYYRLYNTLD  
DLLLYINARELRITYGQGSGTAVYNNNMYVNM YNTGNIARVNLTNTIAVTQTLPNAAYNNR  
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF  
MVCGLYATRTMNT RTEEIFYYYDTNTGKEGKL DIVMHKMQEKVQSINYNPFDQKLYVYNDG  
YLLNYDLSVLQKPQ

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**FIGURE 39**

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC  
CCTCCTCCCCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT  
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC  
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG  
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT  
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACATGTACGTCAACA  
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

**FIGURE 40**

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT  
 CCGCTGCTCTTGTGACGTTGTGGAG**ATG**GGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCT  
 GGATACCATGTTTGTGTGGAAGTGCCCGTGTGCTATGCCGATGCTGTCTTAGTGGAAC  
 AACTCCACTGTAAGTAGATTGATCTATGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTG  
 TGTAAATGTTGATACCAGGAATGGAAGAACAAGTAATAAGATTCTGGATTTTGTGAGAATG  
 AGAAAGGTGTTGTCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT  
 GGTTTGGCTATGTTCTATCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA  
 TCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTA  
 TTATTGGGGCATTCTTCATTCCAGAAGGAACTTTTACAAGTGTGTGGTTTTATGTAGGCATG  
 GCAGGTGCCTTTTGTTCATCCTCATACAAGTAGTCTTACTTATTGATTTTGCACATTCATG  
 GAATGAATCGTGGGTTGAAAAATGGAAGAAGGGAAGTCTGAGATGTTGGTATGCAGCCTTGT  
 TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTCTTCTTGTCTAC  
 TACACTCATCCAGCCAGTTGTTTCCAGAAAACAAGGCGTTTATCAGTGTCAACATGCTCCTCTG  
 CGTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTT  
 TGTTACAGTCTTCCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT  
 GAACGAGAAACAAATTGCAACCCAAAGTCTACTAAGCATAAATTGGCTACAATAACAAGCAC  
 TGTCCTCCAAAGGAAGGGCAGTCAGTCCAGTGGTGCGATGCTCAAGGAATTATAGGACTAATTC  
 TCTTTTTGTTGTGTGATTTTATTCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAA  
 CTGACTCTAACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATC  
 ACTGGAGGATGGGGACGATGTTTACCCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA  
 GTTATTCTTCTTTCACCTCATGCTTTTCTGGCTTCACTTTATATCATGATGACCCTTACC  
 AACTGGTCCAGGTATGAACCCCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA  
 AATCTCTTCCAGTTGGATTGGCATCGTGCTGTATGTTTGGACACTCGTGGCACCCTTGTTC  
 TTACAAATCGTGATTTT**GACTGAG**TGAGACTTCTAGCATGAAAGTCCCACTTTGATTATTGC  
 TTATTTGAAAACAGTATTCCCAACTTTTGTAAAGTTGTGTATGTTTTTGTCTCCCATGTAAC  
 TTCTCCAGTGTTCTGGCATGAATTAGATTTTACTGCTTGTCAATTTTGTATTTTCTTACCAA  
 GTGCATTGATATGTGAAGTAGAATGAATTGCAGAGGAAAGTTTTATGAATATGGTGATGAGT  
 TAGTAAAAGATGGCCATTATTGGGCTTATTCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA  
 ACAAATTTGTTTACTATTTTAAAATTATATTAGACCTTAAGCTGTTTTAGCAAGCATTAAA  
 GCAAATGTATGGCTGCCTTTTGAATATTTGATGTGTTGCCTGGCAGGATACTGCAAAGAAC  
 ATGGTTTATTTTAAAATTTATAAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA  
 AGTTTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGACAATAGTGTAGG  
 TTATGGATGGAGGTGTCCGTACTAAATTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA  
 TGGCCTTTGCCAACAAAGTGAAGTGTGTTTGGTTGTTTTAACTCATGAAGTATGGGTTCACT  
 GGAAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGA  
 AGGAAGTGTTTTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCAGCACGGTAGCTCACCTT  
 GGAATCCAGCACTTTGGGAGCTTAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACCA  
 GCTTGGCACATGGTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCCTGTGGTC  
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGGTTGCAGTGAGCAAGTCA  
 CGTCACTGCACTCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATATTGAAATCAAGG  
 AGGCAAAATTTTACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTAT  
 ATAAAATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA  
 GCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATAATAGCATTCTCTCTGACATTTAA  
 AAATAATTTCTATTCAAATACATGCATATTGATTTACACCTCATACTGTGATAATTAATGT  
 GATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAAGAATGATGGAATGTTTT  
 AGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAGATGTTTAAAAATGCTTTTGTAT  
 TTACTGCCATGTAATTGAAATATATAGATTATTGTAACCTTTCAACCTGAAAATCAAGCAGT  
 ATGAGAGTTTAGTTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAAAATCTACAATT  
 TCTTCTTTAAAAATATTTATTAATGTGAATGGAATATAACAATTCAGCTTAATCCCCAAC  
 TTATTCTGTGTGTAGACATTGTATTCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAA  
 ATGAATTCAGAGAAAAA

**FIGURE 41**

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME  
EQLNKIPGFCENEKGVVPCNILVGKYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG  
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKM  
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI  
LPKIQESQPRSGLLQSSVITVYTMylTWSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV  
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH  
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVVKISSSWIGI  
VLYVWTLVAPLVLTNRDFD

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**FIGURE 42**

[illegible]

**FIGURE 43**

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC  
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNTATGCCGATGCTGTCCTAGTGGAACAANTCC  
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTTGGAGTANGTGTAGCTTGTGTAAT  
GTTGATAACCAGGAATGGAAGAACAACCTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG  
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG  
GCTANGTTCTATNTTCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG  
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG  
GGGC

**FIGURE 44**

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC  
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT  
TGCTATGCCGATGCTGTCCTAGTGGAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT  
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC  
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG  
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTA  
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT  
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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**FIGURE 45**

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACTTTTTTCCTTG  
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA  
AGATTCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC  
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTTACT  
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT  
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT  
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAC TAGT  
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA  
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA  
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC  
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

**FIGURE 46**

CTCGGGCGCGCACAGGCAGCTCGGTTTGGCCCTGCGATTGAGCTGCGGGTTCGCGGCCGGCGCCGGCCTCTCCAAT  
GGCAAATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTTCGGCAAAGGCAGTCGAGTGTTCGAGACCGGGGCGAG  
TCCTGTGAAAGCAGATAAAAAGAAAACATTTATTAACGTGTTCATTACGAGGGGAGCGCCCGCGGGGCTGTGCG  
ACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGCAGATTAC  
GTCGTTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTTATTAGCGATGCC  
CCCTGGTTTGTGTGTTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCC  
TGGGCGAATCCCACATCTGTTTCACTCTCCGCCGAGGGCGAGCAGGAGCGAGAGTGTGTGAATCTGCGAGTG  
AAGAGGGACGAGGGAAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAAGAACACCAGAT  
CAGCAAAAAAGAAAGATGGGGCCCCCGAGCCTCGTGCTGTGCTTGTGCTCGGCAACTGTGTTCTCCCTGCTGGG  
TGGAAGCTCGGCCCTTCTGTGCGACCACCGCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCCA  
ACATCATCCTGGTGCTGACGGACGACCAGGATGTGGAGCTGGGTTCATGCAGGTGATGAACAAGACCCGGCGC  
ATCATGGAGCAGGGCGGGGCGCACTTCATCAACGCCTTCGTGACCACACCCATGTGCTGCCCTCACGCTCCTC  
CATCCTCACTGGCAAGTACGTCCACAACCACAACCTACACCAACAATGAGAACTGCTCCTCGCCCTCCTGGC  
AGGCACAGCAGAGAGCCGCACCTTTGCGGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG  
TATCTTAATGAATACAACGGCTCCTACGTGCCACCCGGCTGGAAGGAGTGGGTGCGACTCCTTAAAACTCCCG  
CTTTTATAACTACACGCTGTGTGGAACGGGGTGAAGAGAAGCACGGCTCCGACTACTCCAAGGATTACCTCA  
CAGACCTCATCACCATGACAGCGTGAGCTTCTTCCGCACGTCCAAGAAGATGTACCCGCACAGGCCAGTCCTC  
ATGGTCATCAGCCATGCAGCCCCCAGGGCCTGAGGATTACGCCCCACAATATTCACGCCTCTTCCCAAACGC  
ATCTCAGCACATCAGCCGAGCTACAACACGCGCCCAACCCGGACAAACACTGGATCATGCGCTACACGGGGC  
CCATGAAGCCCATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGACAGACCTCATGTGCGTGGAC  
GACTCCATGGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACCCGC  
CGACCACGGTTACCACATCGGCCAGTTTGGCCTGGTGAAAGGGAAATCCATGCCATATGAGTTTGACATCAGGG  
TCCCGTTCTACGTGAGGGGGCCCCAACGTGGAAGCCGGCTGTCTGAATCCCACATCGTCCTCAACATTGACCTG  
GCCCCACCATCCTGGACATTGACGGCCTGGACATACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCT  
GGACACGGAGCGGCCGGTGAATCGGTTTCACTTGAAAAAGAAATGAGGGTCTGGCGGACTCCTTCTTGGTGG  
AGAGAGGCAAGCTGCTACACAAGAGAGACAATGACAAGGTGGAGCGCCAGGAGGAGAACTTTCTGCCAAGTAC  
CAGCGTGTGAAGGACCTGTGTGACGCTGCTGAGTACCAGACGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTG  
TGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGCAAGGGCCCCATGCGGCTGGGCGGCAGCAGAGCCC  
TCTCCAACCTCGTGCCCAAGTACTACGGGCAGGGCAGCGAGGCCTGCACCTGTGACAGCGGGGACTACAAGCTC  
AGCCTGGCCGGACGCCGAAAAAATCTTCAAGAAGAAGTACAAGGCCAGCTATGTCCGCAGTCGCTCCATCCG  
CTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCACGTAGGCCTGGGTGATGCCGCCAGCCCCGAAACCTCA  
CCAAGCGGCTGCGAACAACGACACGTGCAGCATGCGAGGCCTCACGTGCTTCACCCACGACAACCGACTGG  
CTTCCCGACTACTCAGCCGCCAACCCCATTAAGTGACACATCGGTGCTACATCCTAGAGAACGACACAGTCCA  
GTGTGACCTGGACCTGTACAAGTCCCTGCAGGCCTGGAAGACCACAAGCTGCACATCGACCACGAGATTGAAA  
CCCTGCAGAACAAATTAAGAACCTGAGGGAAGTCCGAGGTACCTGAAGAAAAAGCGGCCAGAAGAATGTGAC  
TGTCACAAAATCAGCTACCACACCCAGCACAAAGGCCGCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTCAG  
GAAGGGCCTGCAAGAGAAGGACAAGGTGTGGCTGTTGCGGGAGCAGAAGCGCAAGAAGAACTCCGCAAGCTGC  
TCAAGCGCTGCAGAACACGACACGTGCAGCATGCGAGGCCTCACGTGCTTCACCCACGACAACCGACTGG  
CAGACGGCGCCTTTCTGGACACTGGGGCCTTTCTGTGCTGCACCAGCGCCAACAATAACACGTACTGGTGCAT  
GAGGACCATCAATGAGACTCACAATTTCTCTTCTGTGAATTTGCAACTGGCTTCTTAGAGTACTTTGATCTCA  
ACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACTGGACAGGGATGTCTCAACCAGCTACACGTACAG  
CTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGGACCTGGATGGAGG  
AAGCTATGAGCAATACAGGCAGTTTCAGCGTCGAAAGTGCCAGAAATGAAGAGACCTTCTTCAAATCACTGG  
GACAACCTGTGGGAAGGCTGGGAAGGTTAAGAAACAACAGAGGTGGACCTCCAAAAACATAGAGGCATCACCTGA  
CTGCACAGGCAATGAAAAACCATGTGGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGGAGGCCTGAGAAAGC  
AAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCC  
ATTTTTGCCCTGCTTTTGGATTATACCTCACCAGCTGCACAAAATGCATTTTTTTCGTATCAAAAAGTC  
ACCACTAACCTCCCCAGAAGCTCACAAAGGAAAACGGAGAGAGCGAGCGAGAGAGATTTCTTGGAAATTTT  
TCCCAAGGGCGAAAGTCATTTGGAATTTTAAATCATAGGGGAAAAGCAGTCTGTCTAAATCCTCTTATTCTT  
TTGGTTTGTACAAAGAGGAACCTAAGAAGCAGGACAGCAACCTGGAGAGGCTGAAAACAGTCGAGAGACG  
TTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACTATAAACCTGGTTGCTCTGAAGAAA  
CTGCCTTCATTGTATATATGTGACTATTTACATGTAATCAACATGGGAACCTTTTAGGGGAACCTAATAAGAAAT  
CCCAATTTTCAGGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGTAAAAGAAAAA

**FIGURE 47**

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPNIILVLTDDQDVELGSMQ  
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGYVHNHNTYTNNENCSSPSWQAQHE  
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD  
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP  
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT  
YIVYTADHGYHIGQFGLVKGKSMPIYEFDIRVPPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI  
AGLDIPADMKGKSLKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN  
FLPKYQQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKY  
YGQGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAI EVDGRVYHVGLGDAAQ  
PRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS  
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSL  
HPFRKGLQEKDKVWLLREQKRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG  
PFCACTSANNNTYWCMRTINETHNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL  
HVQLMELRSCKGYKQCNPRTNRMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

**FIGURE 48**

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA  
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC  
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCCTGCTGCTGCTGCTGCTGCTGGCCACC  
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA  
CCGAGTCCGCCGGGGCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC  
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC  
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA  
CGCTCGCTTGAGGCTGCTGTGCGCCGGTGCCTGTGGACAGCAGCTGCCCCCTGCCCTCCCATCTG  
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG  
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC  
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG  
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG  
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC  
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT  
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTCATCGGTGCCTTAGTCCAAGAAAAT  
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 49**

MLGLLGSTALVGWITGA AVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRRAQPWPFR  
RRGHLGIFHHHRHHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

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**FIGURE 50**

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTA  
CTACTGGGCCTGATTGGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG  
GTACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA  
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC  
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC  
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC  
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC  
CATGTGGTGACAGCCACCTTCCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG  
TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG  
AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT  
GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA  
GGTGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCC  
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACCTGGGGCGAGCAGCCGTGGCTGGGAT  
GACGGTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA  
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC  
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCCTGAGAAGGGCAAGGAGTAACCC  
ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT  
CCAGCCCTCTTCTCCTTCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC  
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA  
GGGACTATTTTCTGCACCAGCCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC  
ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTTCACCTGGAAAAAA  
AAAAA

**FIGURE 51**

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR  
LFTESCSISPKLRSIAYYYDNPHMVPPDKCRAVGSI LSEGEESPSPELIDLYQKFGFKVFS  
FPAPSHVVTATFPYTTILSIWLATTRVHPALDITYIKERKLCAYPRLEIYQEDQIHMCPLAR  
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAA TLSPGAS  
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK  
GKE

**FIGURE 52**

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT  
GCCCCGCGCCCAGTCA**ATG**ACCCTGCGCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT  
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA  
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGA  
GACACGCTTCACATACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT  
GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA  
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT  
GGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT  
GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAG  
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT  
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAA**TA**  
**ATAAATAATAAATTTTAAAAAACTTAAAAA**



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**FIGURE 53**

MTLRPSLLPLHLLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFCDTLHI  
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF  
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS  
KKKLKEEKRNSKKK

**FIGURE 54**

CCCGGGAACGTGTTCTGGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC  
CCCGCGCCCAGTCATGACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC  
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC  
CTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA  
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA  
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT  
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG  
AAAACGGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA  
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG  
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA  
CCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA  
AATAATAAATTTTAAAAAACTTA

**FIGURE 55**

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCC  
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG  
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA  
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT  
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT  
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG  
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC  
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAA  
CAAGAGCAAAAAGAAATAATAAATAATAAATTTTAAAAAACTTAAAA

**FIGURE 56**

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGGAG  
TGAGGCGGGCCGGCGCGGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG  
ACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG  
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT  
TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT  
GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA  
GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG  
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG  
CTAAAGAAAAAGACATAGTATAACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT  
TTTGGAGGGCTGGTTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT  
TTCCACAGCACAACAGCCCTGCATGGGTTTGTGTTGTTTTTTTACTGCTCACTCCCAACCTT  
TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT  
AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACTTGATTAACCT  
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT  
TGTA AAAAATAAAAAGAAATTACAAAAGAAATTATGGATTTGTCAATGTAAGTATTTGTCATA  
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT  
CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTTAGTTTTTTAAATATTCCGTGG  
TCAAATTCCTCCTCACTATAATTGGTATTTACTTTTACCAAAAATTCTGTGAACATGTAAT  
GTA ACTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT  
GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT  
CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC  
CACATCCACCACTG

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**FIGURE 57**

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLF'FTGWWIIIIDAAVIYPTMKDFNHSYHACGVI  
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK  
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

**FIGURE 58**

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGGCCGGCGCGGCGCGACACCGGGCTCCGGAACC  
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG  
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC  
TATTTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT  
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC  
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG  
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG  
ATTCTTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT  
TTTCCAGAATGCCTTCATCTTTTTTTGGAGGGCTGGTTTTTTAAGTTTGGC

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**FIGURE 59**

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTTCTAGAATGCATGAC  
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG  
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC  
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA  
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT  
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT  
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC  
ATCTTTTTTGGAGGGCTGGTTTTTAAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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**FIGURE 60**

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT  
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT  
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT  
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC  
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGT  
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT  
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT  
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC



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**FIGURE 61**

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGGAAAAGCGCAATANTATTGCTTCC  
ATTGNTGNTGGTGTANTATTTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT  
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC  
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG  
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN  
TGATTGCATTTTATGTGGATTNTTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC  
CCTGT

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**FIGURE 62**

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGCCCCGGCGCGG  
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAATGTTTG  
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT  
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT  
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA  
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA  
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG  
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG  
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

**FIGURE 63**

CGACGCCGGCGTG**ATGT**GGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGGCCGTCC  
TCTGCAAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC  
AAACGGCCCCCAGCGCCCCCTGGTAAGTACAAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC  
TTTTTTCAGCCAACCAAGTGCCGAGAAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG  
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCCTGGTGCTGGAACAACAT  
ACCAAGGCAGGGGGCTGCTGTACATCCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAAT  
CCATTACATTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTTATCTTGGACCATCACTG  
AAGGGCAGCTGGACTGGGCTCCCCGTGCTCTCTCTTTTGACATCATGGTACTGGAAGGGCCC  
AATGGCCGAAAGGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTCAGGGCCTCAAGGA  
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA  
GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTGCCCCGTGGTTCAGCTCCTCGAC  
AGGTGTGGGCTGCTGACTCGTTTCTCTCATTCTTCAAGCATCCACCCAGAGCCTGGCTGA  
GGTCCTGCAGCAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA  
CTTACGGTGTACCCCCAACACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTAC  
ATGAAAGGAGGCTTTTATCCCCGAGGGGGTTCAGTGAAATTGCCTTCCACACCATCCCTGT  
GATTTCAGCGGGCTGGGGGCGCTGTCCTCACAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT  
CAGCTGGGAAAGCCTGTGGTGTGCTGAGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC  
CCCATCGTGGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC  
CCGCTGCCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGCGGCCCGGCTTAGGCATGACCT  
CTGTTTTTCATCTGCCTGCGAGGCACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTAT  
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGCTACGTCTCCATGCCCAGGGAAGA  
GGCTGCGGAACACATCCCTCTTCTCTTCTCGCTTTCCCATCAGCCAAAGATCCGACCTGGG  
AGGACCGATTCCCAGGCCGGTCCACCATGATCATGCTCATACCCACTGCCCTACGAGTGGTTT  
GAGGAGTGGCAGGCGGAGCTGAAGGGAAGCGGGGACGTGACTATGAGACCTTCAAAAACCTC  
CTTTGTGGAAGCCTCTATGTGAGTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGG  
AGAGTGTGACTGCAGGATCCCCACTCACCACCAAGTCTATCTGGCTGCTCCCCGAGGTGCC  
TGCTACGGGGCTGACCATGACCTGGGCCGCTGCACCCTTGTGTGATGGCCTCCTTGAGGGC  
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTGTGGACTGGTCTG  
GGGCCCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCCTGAAGCGGAACCTGTACTCAGAC  
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAAT**TAG**TTCCATCAGGGAGG  
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG  
CATTAGTTCCTTGACGTATAAAGCACTCTAATTTGGTTCTGATGCCTGAAGAGAGGCCTAG  
TTTAAATCACAATTCGGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA  
TCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG  
TCTCATGACGAGCGGCGCTCTGCATCCCTCACCCATGCCTCCTAACTCAGTGATCAAAGCGA  
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTCAGCTCAACCTGGTGGGTTCAAGTTC  
TGTCCTGAGGCTTCTGCTCTCATTCAATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG  
GAAAAGGGGAGACTAATGAGGCTTAACTCAAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA  
GGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCAAGTGGCTCTTTCAGGGGACAGGAAAT  
GCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA  
GGGTGCATGTCAGATGATCATATCCAATTCATATGGAAGTCCCGGGTCTGTCTTCTTATCA  
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGC  
CTTATCCACCAATAACACAGGGAAGGGTGATGCAGGGAAGGGTGACATCAGGAGTCAGGGCA  
TGGACTGGTAAGATGAATACTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCCAGCCAAGGG  
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAGTCACATCAGAAAAGGGA  
AAGCCACGGAATGTGTGTGAAGCCCAGAAATGGCATTGTGAGTTAATTAGCACATGTGAGGG  
TTAGACAGGTAGGTGAATGCAAGCTCAAGTTTTGGAAAAATGACTTTTCAGTTATGTCTTTG  
GTATCAGACATACGAAAGGTCTCTTTGTAGTTTCGTGTTAATGTAACATTAATAAATTTATTG  
ATTCCATTGCTTTAAAAA

**FIGURE 64**

MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKARKKVLKQAFSAN  
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG  
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQ  
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ  
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA  
GGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP  
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYYDTDMDQAMERYVSMPREEAAEH  
IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEA  
SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI  
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

[illegible]

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**FIGURE 66**

MRVRIGLTLLLCVLLSLASASSDEEGSQDES LDSKTTLTSDSVKDHTTAGRVVAGQIFLD  
SESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG  
EPCHFPPFLFDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMQEAMM  
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMF EK  
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

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**FIGURE 67**

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT  
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT  
GTCAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG  
CTCAACTCTCCTGCACGCTCAGCCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCCTGG  
TACCAGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA  
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCT  
GTGTCCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC  
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT  
GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG  
TTAATAATATTCAACATGTCAACAAC

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**FIGURE 68**

MACRCLSFLLMGTFLSVSQTIVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG  
SAPRYLLLYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPQPEDDADYYCSVGYGFS



**FIGURE 69**

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**FIGURE 70**

MTPSPILLLLLLPPLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM  
WTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDLDDISPGK  
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIA RPVGSSVRLKCVASGHPRPDITWMK  
DDQALTRPEAAEPRKKKWTL SLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL  
TGTHPVNTTVDFGGTTSFQCKVRS DVKPIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD  
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA  
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS  
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHHTSHSHVEGKV  
HQHIHYQC

FIGURE 71

**FIGURE 72**

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI  
DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQ  
RPGQNCNSNYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS  
EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAIYLLTK  
TPKLLTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY  
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLKQQHQAG  
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQATNSFYDVGRCPV  
KTCAGQQDNGIRCRDAVQNCCGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRIVRGRV  
SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNNTTKVLPFN  
KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV  
KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL  
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLENL  
DVPESRRRCFVKVRAYRSERFLPSEQIQGVVISVINLEPRTGFSLNPRAWGRFDSVITGPNGA  
CVPAFCDDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRRTDHEDPR  
VKKTAFAQISMAKPRPNSAEESENGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPVFN  
EDDPMSWTEGYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS  
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVKVIPQGSRRASVNPMLHEYLVNHLPLAV  
NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSBGSSRIMKSNVGVALT  
FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA  
QQPLIN

**FIGURE 73**

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC  
AATATCTTAACTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG  
ACCTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACTAGACAAAGATCGCAGATCATAAAGC  
AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAAGAATTTAGAGATGATTTGTCAAGATCCCTGTGATTTCATG  
CCCTTTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCCTTTGGTTTGGGGACATTATGATTTGTGTAAGACT  
CAGATTTACACGGAAGAAGGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATA  
TCTGAAAGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCTCCTGAGACGTTCTGTGCAATGGGCAATC  
CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGATTTT  
GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAAAGGAGTATCCCAAGCCTCTCCAGGTTAAT  
CACTCTGTCTTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC  
AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA  
GATGCTTTTTACATGGATCCTAAATCCGTGAAGGATTTATCACAGCATACGGTCTTAGAAATCATTGTCACAGA  
AGAGTACTCAACAGGGTATACAACAAATAGCAAAATATCCACTTTGAAATCAAAGACAGGTTGCGCTTTTTG  
CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT  
ACAGTCACAGACCTGAGGATAAAGCTGTAAAGACCAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGC  
ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCTCCATGCCACTGTATGTG  
TGTATGACAACAGCAAATTGACATGCGAATGTGAGCACAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAG  
AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCACTGCAAATACCTGTATCCC  
CAGTATTTCCAGTATTGGTACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGAGCTGCCACA  
ACAACGTGCGCTGCGTGTGCCCGGCCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC  
AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCCGCACGGCACCCCCAGCGCTGCTGCTGCTGACCACGCTGCT  
GGGAACCGCCAGCCCCCTGGTGTCTTAGGTGTACCTCCAGCCACACCGGACGGGCCTGTGCCGTGGGGAAGCA  
GACACAACCCAAACATTTGCTACTAACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAA  
CTAAGAAGGCCTAACTGAACCTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTT  
TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAATCACATTGCCAGCTGCAGAGCATATTGTGGA  
TTGGAAAGGCTGCGACAGCCCCCAACAGGAAAGACAAAAACAAACAAATCAACCGACCTAAAAACATTGGC  
TACTCTAGCGTGGTGCGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTCAG  
GTGCATTGTGGGCATAAGGAAATCTGTTACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC  
CTGTGCTTTAGTGAACGTTGCTCTGTAACCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACA  
TGTGTAACAGCCCCCTCTAAAAGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA  
GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTT  
ATTTTTCTTGAACCTACTGTAATATGTAGATTTTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAAT  
GTATCTAATTGCAATCAGCAAAGACTGACATTTTATTTTGTCTCTTTTCTGTTTGTGTTTCACTGTGCAGA  
GATTTCTCTGTAAGGGCAACGAACGTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGTGTAAATAAGA  
TTCCACCAAAGGACATTCTAAATGTTTTCTTGTGCTTTAACACTGGAAGATTTAAAGAATAAAAACTCCTGCA  
TAAACGATTTTCAAGAAATTTGTATTGCAATTTCTTAAGATGAAAGGAACAGCCACCAAGCAGTTTACACTCACT  
TTACTGATTTCTGTGTGGACTGAGTACATTGAGCTGACGAATTTAGTTCCCAGGAAGATGGATTGATGTTCACT  
AGCTTGGACAACCTTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAA  
AAAAAA

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## **FIGURE 74**

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK  
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK  
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCCLDAF  
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD  
TTKKLRDFFTVDLRLRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN  
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPKPGTANTCIPSISSIGTNVCDNELLH  
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS  
PLVF

**FIGURE 75**

CCCACGCGTCCGGGTGACCTGGGCGGAGCCCTCCCGGTCCGGCTAAGATTGCTGAGGAGGCGG  
CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGTCCGGGCGAGGTGTCTCATGACTT  
CTCTTGTGGACCATGTCCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC  
CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGGGAATGGAGGAGACGGCTCA  
AGAGTTTAGCCTTGCGACTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT  
AGTATACATTTTTTCTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC  
AGCAGCCATGGCCTTCTGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCTATGACA  
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTAG  
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAAT  
TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA  
ATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA  
CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT  
CATTCGAGGAGTTCACCTTGCGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT  
TGGACCAAACCTCGTTGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT  
CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA  
AAAGGGCATGTCAGTGAAATCTGGGAATGGCTGGATTCCGAAACATCTGCCCATGTGTATTG  
ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTTAGGGTAAAATTAACAAATCCATTCTAT  
TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCTTACATTTATATGATTCTGGGGTT  
GCTTCAGAAGTGTTATTTTCATGAATCATTTCATATGATTTGATCCCCCAGGATTCTATTTTGT  
TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT  
TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTTC  
TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAAACTCAGTAGTACAACC  
TAACTTGTATAAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAAATG  
AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAATAAAAAAAAAAAAAAAAAAA  
AAAAG

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**FIGURE 76**

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIF  
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW  
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA  
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS



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## **FIGURE 77**

TGCTTCCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGC  
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT  
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG  
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

**FIGURE 78**

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA  
CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAAACGAGGCGGGTGGTG  
CCTGCCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT  
TCTGTGCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCTT  
CCTCCCCGCTCGTCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA  
**TG**GGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC  
GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGAC  
CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA  
TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCC  
TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACACTACTACATCCAGTGGCT  
CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTTCTCTTCCCCAACCTGTCCCTCA  
TCTTCCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG  
GGTGTCTGCGGGCCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT  
AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT  
ATGACTTTTGGGAGTACTATCTCCCCTACCTCTACTCATGCATCTCCTTCCTTGGGGTTCTG  
CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT  
AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG  
CAGCCCTGACCCGCAGGATCTGTAATCCTACTTCCTGCTGGCTGCCTTTAGACATGGAGCTG  
CTACACAGACAGGTCCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC  
TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGGTGCTGACGG  
GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG  
CCCCGAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG  
TGCCGTCAATTCAGGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTATA  
GCTCTCCACTCTTCCGGAGCCTGCGGGCCAGATGGCACGACACTGCCATGACGCAGATAATT  
GGGAACGTGTGTCTGTCTCCTGGTCTTAAGCTCAGCACTTCCTGTCTTCTCTCGAACCTGGG  
GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA  
TTGTGTTCTCTACAACGCAGCCTTTTGAGGCCTCACCACACTCTGTCTGGTGAAGACCTTC  
ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCTTTGGGCTGGACAGACTGCCGCTGCCCGT  
CTCCGGTTTCCCCCAGGCATCTAGGAAGACCCAGCACCA**GTGA**CCCTCCAGCTGGGGGTGGGA  
AGGAAAAAACTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGG  
ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATT  
GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAAGTGTGGCCT  
CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCCTGATCCCAAATCTGTTTACACATCA  
ATCTGCCTCACTGCTGTTCTGGGCCATCCCATAGCCATGTTTACATGATTTGATGTGCAAT  
AGGGTGGGGTAGGGGCAGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC  
CTTGCCCTCTGGCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTG  
AAAGACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCCAGGGA  
AAAAAA

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**FIGURE 79**

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVVK  
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSL  
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL  
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMF SVTGKLLVKPRLLEDLEEQLYCSAFEE  
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT  
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFAGVIQVVLI FYLMVSSVVG FY  
SSPLFRSLRPRWHD TAMTQIIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLG NFY  
IVFLYNAAFAGLTTLCLVKTF TAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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**FIGURE 80**

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC  
GCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC  
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA  
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC  
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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## **FIGURE 81**

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC  
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC  
TGTCGCAGGCTGCGAGGAAAGGCCCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT  
CCCCGTTGTCNTCCCCGGGCCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA  
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT  
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC  
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC  
GCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT  
CCATCATCAGCAATGAGGTGCTGCACTCCC

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**FIGURE 82**

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT  
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCATGCTGCTGT  
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCCATT  
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGCAA  
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA  
TACTAAGAGAAAACCCAGACAATATCCTTGAGGTTGAGGAATCTGGAGAGTACAGATGCCAG  
GCCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC  
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCTTAGGCCTCTC  
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC  
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA  
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA  
AAA

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**FIGURE 83**

MLLVVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQTKWYHRYL  
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDSESSEMGFPHAAQANVELLGSSDLLT

**FIGURE 84**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGT  
GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG  
GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT  
GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG  
GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA  
GCTTCATCCCGACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG  
CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA  
GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTT  
TGGTTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA  
TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT  
AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACCGGAAGTGCAATTGTGCGCAAGAGAT  
GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT  
GCCCTAATGTCAAAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG  
AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG  
AGATTTACGGTTCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT  
TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT  
CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT  
ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA  
TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA  
CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG  
AATAAAATTGGACTTTGTTTAAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT  
TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA  
TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTTCGGAAAAGAAATGACC  
AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGT  
TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA  
GTTGTTAGCAATTTCAATCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG  
TTATTTT



**FIGURE 85**

MAPQNLS TFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRK LALQLHPDRNPDDPQ  
 AQEK FQDLGAAYEVLSDSEKRKQYD TYGEEGLKDG HQSSHGDI FSHFFGDFGFMFGGT PRQQ  
 DRNIPRGSDI IVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ  
 MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGM EYPFFIGEGEPHVDGEPGDLRFRIKVVKH  
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHK V HISRDKITRPGAKLWKKGEGLPNFD  
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

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**FIGURE 86**

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA  
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT  
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG  
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAAAAGG  
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCTGATGATCCACAAGCCCAG  
GAGAAATTCCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA  
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT  
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA  
AATATTCCAAGAG

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**FIGURE 87**

GGCACGAGGCGGCGGGGAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT  
CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA  
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**  
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGACGCC  
TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC  
TAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC  
TGGACGATGTCGTTATCACCACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC  
GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC  
AGAGAAGCTTGTTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA  
GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG  
TACCCTCCGTTGGACCCCCAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCAG  
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC  
AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG  
CCAGATAAAGGCCTCCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATT**TAGT**GCCT  
ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT  
CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG  
TAAAGCAGGAGATCCCCGTGAGTTTATGCCTCTTTTGCAAGAGGAGTATTGAAAA  
GTCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACCTCTCTGCAAGAGGAGTATTGAAAA  
CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT  
AAGAAATCAAGAGGTTTCACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAAATG  
TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC  
TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT  
GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAACT  
ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG  
GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

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**FIGURE 88**

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL  
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSAS  
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI  
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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**FIGURE 89**

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTCCGAGGTGCTTTCGCCGCTGTCC  
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA  
TTTGGAGTGTTTTCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT  
TGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTCAGAT  
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTC  
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTTCAG  
GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT  
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA  
AGTGAATTTGAAGACTCATTTAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA  
GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG  
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA  
ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA  
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA  
CTGTGGTGCCTGTTTCTTTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT  
TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA  
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAACCAAGGAAACCCCAATTTTG  
ATGTATGGATTACTTTTTTTTTGNGCNCAGGGCC

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## **FIGURE 90**

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK  
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFI RRVPVLGSLLNLPGI  
RSFVDKVGESNNMV

### **Important features:**

#### **Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

#### **N-myristoylation sites.**

amino acids 11-16, 51-56 and 116-121

#### **Aminoacyl-transfer RNA synthetases class-II protein.**

amino acids 49-59

**FIGURE 91**

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC  
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA  
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTGTTCTTTGGA  
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT  
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAACATAAAATGAAAG  
CTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG  
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

**FIGURE 92**

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA  
GGCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGA  
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC  
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC  
ATCAACACCATTTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA  
GATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT  
CGGGCACGGAATGCACCATCTTCACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAT  
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA  
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA  
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT  
CGAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTTCCT  
GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC  
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC  
ACCGTGAGGAGCTTGAGAAATGTAGTTTTCAGCTGTATATGACTGTACACTCAATTTAGAAA  
TAATGAAAATCCAACACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATG  
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC  
AAGCTCTACCAGGAGAAGGATGCCTTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA  
GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCCTCGTGAACCTGGCTGTTTTGGGCCTCGC  
TGGTGCTCTACCCTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG  
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT  
GACGGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT  
GACTCAGGGAGGTGTCACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT  
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTCACGA  
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT  
TTTTCCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC  
TGTGTGGTGAGTGTGAACTTTGTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG  
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCCTTTCATCCTTTGGTGCTGAGTTTTCTGT  
AACCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC  
CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAA



**FIGURE 93**

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLV  
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGGSKVLAKK  
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHE  
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVNLGKK  
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN  
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRRMIGVTEIDKGSAYGNSDS  
KQKLND

**FIGURE 94**

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTGCGCGGTGCTCTCGGGCTTTGTGCTCG  
GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA  
GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA  
TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG  
GCGAAGTAAATGAGCAAGCACTGAAGAAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT  
TGGTACAAATTCCGTCGTCATTTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA  
AACTTGCAGGAGCATTTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAA  
TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT  
TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTTATAAAAC  
TGTATCAGGTTCCCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT  
TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA  
CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACT  
AGTAAAGGATGTAAACAGATTAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGG  
CAGCAAGAGAGAAGAACATCCAAAAAGACCCTCAGGAGAACATTTTTCTTTGTTCAGGCATTA  
CGGACCTTTTTTCCAAATTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA  
TGTTTCTAAAAGTAGCTGTAACCTACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA  
TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAGCAT  
AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA  
CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC  
CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA  
TTTTGATCCTTTTAACTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT  
TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTAC  
CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC  
ATCAGATGCTTTTTATTTCCAAACCTTTTTTTTACCTTTCACTAAGTTGTTGAGGGGAAGGCT  
TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA  
TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC  
TGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAAATGGAAAAGCAAGAATAGCCTTAT  
TTTCAAAATATGGAAAGAAATTTATATGAAAATTTATCTGAGTCATTAAAATTCTCCTTAAG  
TGATACTTTTTTGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA  
ATAAATTTGCAAAACATCATCTAAAATTTAAAAAAAAAAAAAAAAAAAAA

**FIGURE 95**

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGGEVKGEAKNSITDSQMDDVEVVYTIDIQ  
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH  
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC  
MSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN  
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS  
CNYNHHLDDVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDLDQDKRSKA  
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

**FIGURE 96**

GGCACAGCCGCGCGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGC  
CCAAGCAGCGCGCAGCGAACGCCCCGCGCCGCCACACCCTCTGCGGTCCCCGCGGCGCCTGCCACCCTTCCCT  
CCTTCCCCGCGTCCCCGCTCGCCGCGCAGTCAGCTTGCCGGGTTCGCTGCCCCGCGAAACCCCGAGGTACCA  
GCCCCGCGCCTCTGCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCCTGGCCCCGGCGCCTGGCACC  
GGGGACCCTTGCTGACGCGAGGCCCAGCTCTACTTTTGGCCCCGCGTCTCCTCCGCCTGCTCGCCTCTTCCAC  
CAACTCCAACCTCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAG  
CGCCGCTTCCCGTCCGGTCCCAAAGGTGGGAACGCGTCCGCCCGGCCCGCACCATGGCACGGTTCCGGCTTGCC  
CGCGCTTCTCTGCACCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG  
AAGTGCAGAGTCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT  
TTGAAGATCTGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGA  
TGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTGTCTTACGTTACAAGAAGTTTG  
ATGAATTCCTTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT  
TTATACATGCAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT  
GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCCTGGTGAACCTCCAGT  
ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT  
CGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTCGCTCAAGGCTTAGCGGTTGCGGG  
AGATGTGCTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT  
GCTCCCACTGCCGGGGTCTCGTGACTGTGAAGCCATGTTACAACACTACTGCTCAAACATCATGAGAGGCTGTTTG  
GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA  
GGGTCTTTTCAACATTGAATCGGTCTGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG  
ATAATAGTGTTCAAGTGCTCAGAAGGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATT  
TCTCGTTCCATCTCTGAAAGTGCCTTCAGTGCTCGTTTCAGACCACATCACCCGAGGAACGCCCAACCACAGC  
AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCTT  
CCCTTCCGAGCAACGTTTGAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGG  
AAAGGCAAAAGCAGGTACCTGTTTGCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCA  
GGTTGACACCAGCAAACAGACATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA  
AGAATGCATACAATGGGAACGACGTGGACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGT  
GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGA  
GAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGG  
TTATGCAGAGAGAGTGGAGATTAATTTCTCAAACCTCTGAGAAAAAGTGTTTCATCAAAAAGTTAAAAGGCACAGTT  
ATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAATGGACAACAATGTACAGTTTCTTACTATGTGGC  
CACTGGTTTAAAGAAGTGCTGACTTTGTTTTCTCATTCAAGTTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGT  
TCCTGCTCCCCCAAACCATGTTAAACGTGGCTAACAGTGAGGTACAGAAGTATAGTTAGTTGTGCATTTGTGA  
TTTTATCACTCTATTATTTGTTTGTATGTTTTTTTCTCATTTCGTTTGTGGGTTTTTTTTTCCAAGTGTGATCT  
CGCCTTGTCTTACAAGCAAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATTTCTGAAATATTTAAATA  
GCTGTACAGAAGCAGGTTTTATTTATCATGTTATCTTATTTAAAGAAAAAGCCCCAAAAGC

**FIGURE 97**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRRLYVSKGFNKNDAPLHEINGDHLKICPQ  
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF  
VKTYGHLYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEY  
LECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL  
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES  
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRSESASFARFRPHHPEE  
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLF  
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGE  
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**FIGURE 98**

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**FIGURE 99**

MKVLISL L L L L L P L M L M S M V S S S L N P G V A R G H R D R G Q A S R R W L Q E G G Q E C E C K D W F L R A P R R  
K F M T V S G L P K K Q C P C D H F K G N V K K T R H Q R H H R K P N K H S R A C Q Q F L K Q C Q L R S F A L P L

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**FIGURE 100**

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT  
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA  
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA  
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA  
AACATTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA  
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC  
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC  
CTGACTGCATTTTTGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG  
ATGGAGAGGAAA



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**FIGURE 101**

MAVLVLRRLTVVLGLLVFLTCYADDKPKDKPDDKPDGKDPKPDFPKFLSLLGTEIIENAVE  
FILRSMRSTGFMFDDNEGKHSSK

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**FIGURE 102**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT  
CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCACCTCCTGCAGCTGCTGGTGCTGCTTCTTAC  
CCTGCCCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCC  
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG  
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG  
CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC  
CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT  
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT  
GGTGGTCTGCACTCTGGTGCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC  
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA  
AGCTGGGCCTTCATGTGGCAGCAAGTTTTCTGAGCCCACCTGGAAACACATTGGGGATGGCTG  
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG  
AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC  
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA  
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGAC**CTAG**CAGAATGAGAGAAGACATT  
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC  
CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC  
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC  
CCTTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT  
CTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT  
CTCCCCACTACCACCTTCTTCCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT  
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA  
AACCACG

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**FIGURE 103**

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQL  
KGLTGASGKVALLELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVV  
APGEDMRQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFM  
WQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGPHIMGKAVKQSEF  
SSKALICSFPSLQLEQATHQPIYLPLRGT

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**FIGURE 104**

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG  
CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA  
ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG  
TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG  
TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAAA  
TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG  
AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAAT  
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAG  
TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAGGAA  
AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC  
TTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA  
AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG  
AAGATTGTGATTGAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTAC  
ATTGGCTATCTTGACTATAAAAAGGAAAGAATTCGTAAGCTTTCCATGAAAGCCAGCACTTG  
CTCATTTAATCCTGGAGTTTTTTGTTGCAAACCTGACGGAATGGAAACGACAGAATATAACTA  
ACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT  
GGTAGCATCACAAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC  
TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA  
AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT  
ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCAACCTAATCCGAAG  
ATATACCGAGATCTCAAACATAAAGTGAACAGAATTTGAACTGTAAGCAAGCATTCTCAG  
GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA  
GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC  
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTT  
ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA  
TAATTCAAAACCTGCTGTTGGTTTTTAATTTTGTAACCTGTGGCCTGATCTGTAAATAAACTT  
ACATTTTTTC

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**FIGURE 105**

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGR  
QEEIPVVIAASEDRLGGAIAAINS IQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK  
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT  
ALKPGHAAAFSEDCDSASTKV VIRGAGNQNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA  
NLTEWKRONITNQLEKWMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTIDPMWNVRLGS  
SAGKRYSPQFVKAAKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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**FIGURE 106**

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT  
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT  
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT  
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC  
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA  
TACAAAATTGTCAATTTTGACCCTAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA  
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG  
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC  
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC  
TAAAGTTGTCATCCGTGGAGCAGGAAA

**FIGURE 107**

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG  
GAGCTAGAGGGCAAGTGTGCTCGGCCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC  
TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGGCGCGGGCTGCA  
TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGGCGCGGCGAGCCTTTGAGGGGAACGACT  
TGTCGGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT  
TTCCGATCACTTCAAAGTGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT  
CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC  
CATAACTTCCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTCAGGAATTGTAG  
GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA  
GGAGATTCCGTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA  
ACAGCATTCAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA  
GCAGACCATCTCCGGTCTTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG  
TCAATTTTGACCCTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC  
ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCACAGCGCAAAGAAGG  
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA  
CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT  
CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA  
TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC  
CTGACGGAATGGAAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAACTCAATGT  
AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG  
TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT  
GCTGGAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA  
TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA  
GACCCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA  
CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGGAAG  
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAG  
GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT  
ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA  
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT  
GTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTCAATAGGTAAAAA

**FIGURE 108**

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT  
GAAGGCCGGCCATAACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG  
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC  
GCCATCGTCTGCAACGGTCTCGTGCGCTTCTTGCTGCTGCTGCTGCTGGGTATCCTCTGCTG  
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC  
TGGCCCCTGTCCTGAGAAGGCCCCACCACCCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC  
TGCAGCCCTGAAGGCCCCCTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG  
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT  
TGGAGCTGGACCCAGCGGCCCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC  
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT  
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC  
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG  
GCTGGGCCCCCTCCCCCTGGTCCTCCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA  
AAAAAAAAAAAAAAAAAAAA



FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH  
PRSPAMKAATCCSPEGPWPSLEPRT

**FIGURE 110**

GTTTGAATTCCTTCAACTATAACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA  
GTTCCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA  
CTCCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAA  
TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC  
ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT  
TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC  
TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA  
TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT  
GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC  
AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCCTCTGGGTGGCTGTGCTGCTG  
AGCCTGGGAACTGCAGGAGCTGCCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCCCT  
TTCGGGCATTTCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA  
TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT  
AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA  
AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAATCATTGTCA  
TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA  
TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA  
TACTACAACTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT  
TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTA  
GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG  
GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGCCTACTTAGTAGCCC  
ATAGTTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCCTGTGTTTGTGCTGTTGAT  
CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT  
CGTAAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA  
ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCT  
GGAAAACATTTCCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT  
AGTGAATTTTTTTTTTAAAGACCTAATAAACCCCTATTCTTCCTCAAAA

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**FIGURE 111**

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYDTNDL  
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ  
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI  
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM  
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL  
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH  
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN  
EEGTELQAIVR

[illegible]

**FIGURE 113**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVKAGKIIDPEFIVKC  
PAGCQDPKYHVYGT DVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL  
SLPRWRESFIVLESKPKKGV TYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPV TLMQ  
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQ  
RQDP SGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR  
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTH TNSRDLKTAIEKITQRGGLSNV  
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE  
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKT LQPLVKRVCDTDRLACSKTCLNSADI  
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPD I  
LNAIKRVGYWSSGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG  
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

**FIGURE 114**

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTA  
TGCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT  
GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCCACTACAGTTTTTCTCTGACTCTAAT  
TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG  
TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAAACAAACATT  
CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA  
GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCGAAAACCTCC  
TCCCAGCCTTTTACAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG  
AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC  
CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTTGAAGATGTGGCCAGAGTGGCTTTGATGC  
GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC  
AAGTGGGTGGCCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT  
GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG  
CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAGATGTACAAGGGGACT  
GTGTCCATGCCAGTCTTCCAGTCCTTGGAGGCCTACTGGCCTGGTCTTCAGAGCCTCATTGG  
AGACATTGACAATGCCATGAGGACCTTCCTCACTACTACACTGTATGGAAGCAGTTTGGGG  
GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGGCTACCCA  
CTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT  
CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGCGGAT  
TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCCTG  
GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCACTTCATCCACAACATGG  
GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGGTACA  
TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG  
GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC  
GAAATTTAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC  
TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA  
CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCT  
AGACTCCTCATAACCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA  
AATTGCTTTTGGCTATCATAAAA

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**FIGURE 115**

MPFRLLIPLGLLCALLPQHGGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE  
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLMAEEAARKL  
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM  
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK  
AIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG  
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG  
FATIKDLRDHKL DNRMESFFLAETVKYLYLLEFDPTNFIHNNGSTFDAVITPYGECILGAGGY  
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT  
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

**FIGURE 116**

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
**AATG**CAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCTCTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG  
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT  
GGTCGTGCCACTGTTTCGTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG  
TGGTCCTCCCAGACACCTTGAAAATAACCAATTACCCCAGAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT  
CTCA**TAG**GTTTTGCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC  
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTAG  
TGTTTCTGGAGAGCCCACTTTCCAGATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACCTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTTC  
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAA



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## **FIGURE 117**

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHELLMWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS  
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILIV  
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation sites.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins homology.**

amino acids 92-119

#### **Integrins alpha chain protein homology.**

amino acids 232-262

**FIGURE 118**

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC  
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

**FIGURE 119**

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTG  
GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG  
TCAACATCCGGGGCAAACCTGGTGTCGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG  
AATGTGGCCAGCGAGTGCGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG  
AGACCTGGGCCCCCACCCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG  
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCC  
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA  
GACTTCTGGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG  
TGGTAGGGGCTTGGGACCCAACCTGTGTGTCAGTGGAGGAGGTCAGACCCCAGATCACAGCGCTC  
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATTAACCACCGCGTCTCCTCCTCCACCA  
CCTCATCCCGCCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG  
AGACCCACTGACTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA  
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG  
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA  
TAGAAGTATATCAAGCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC  
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC  
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAAT  
AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT  
GTTATTTCTCCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA  
AACAAATACCTCACGATATAAAATAAAAATGAAAGTATCCTCCTCAAAA

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**FIGURE 120**

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVVNVASECGFTDQ  
HYRALQQQLQORDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG  
AHPAFKYLAQTSKGKEPTWNFWKYL VAPDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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**FIGURE 121**

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC  
TGCGCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCCCGGGCGCCCTCTCT  
CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCCTCAGTTCAGAGAGGTGGATCG  
CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTTCAGGGGTGCACCAAAAAGCATCTTA  
ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC  
TTGGTCGTCCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA  
AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC  
CTAACTCCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCCAGGCGGGCATCATTCTGGTG  
TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCCTCAAGAAGGTGGGCTGCAA  
GGCCCTTGTGTTCCCCAAGCAATTCAGACCCAGCAATACTACAACGTCTGAAGCAGATCT  
GTCCAGAAGTGGAGAATGCCAGCCAGGGGGCCTTGAAGAGTCAGAGGCTCCCAGATCTGACC  
ACAGTCATCTCGGTGGATGCCCCTTTGCCGGGGACCCCTGCTCCTGGATGAAGTGGTGGCGGC  
TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTCTCTGCTGCCATG  
ACCCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGGCCACCCTCTCC  
CACTACAACATTGTCAACAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC  
ACCAGAGCAGTTGCGGATGATCCTGCCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAG  
GCACAATGATGTGTCTGATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGC  
AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGAT  
GTTCTGTGGACATTCTGAACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG  
GTGTCATTGCTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT  
ATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAACAGTCCCCTGACATTCGCGCACTT  
CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGG  
CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGC  
ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT  
GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGGCTTCTGCA  
AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG  
CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA  
CGATCGGATGGGGGAAGAGATTTGTGCCTGCATTTCGGCTGAAGGACGGGGAGGAGACCACGG  
TGGAGGAGATAAAAGCTTTCTGCAAAGGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC  
GTGTTTGTACAAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAAACCTTCGAGA  
GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCCTGTCCTGGCCGGTTGGCTT  
GACTCTCTCCTGTCAGAAATGCAACCTGGCTTTATGCACCTAGATGTCCCAGCACCCAGTTC  
TGAGCCAGGCACATCAAAATGTCAAGGAATTGACTGAACGAATAAGAGCTCCTGGATGGGTC  
CGGGAACCTCGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG  
TCCATCCCCCACATTCCCCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT  
GAAAAAAAAAAAAAAAAA

**FIGURE 122**

MAVYVGMLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLSSREVDRMVSTPIGGLSYVQ  
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG  
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY  
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLP GTLLLDEVVAAGSTRQHLDQLQYN  
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY  
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY  
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG  
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT  
MNEQGFCIVGRSKDMIIRGGENIYPAELEDFHHPKVQEVQVVGKDDRMGEEICACIRL  
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domains:**

amino acids 140-161, 213-229, 312-334

**Putative AMP-binding Domain Signature:**

amino acids 260-271

**N-myristoylation Sites:**

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,  
314-319, 318-323, 379-384, 380-385, 409-413

**N-glycosylation Site:**

amino acids 282-285

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**FIGURE 123**

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA  
TGATCCTGCCCCAACCCCTGTACCATTGCCTGGGTTCCTGTCAGGCACAATGATGTGTCTG  
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC  
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA  
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC  
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT  
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG  
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG  
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT  
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT  
ATTGGACAGGAGATGTCGCCAC

**FIGURE 124**

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC  
AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG  
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC  
GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC  
AGTGCGGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC  
TTCTGGCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC  
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTG  
CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCTGTAGCT  
GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA  
GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA  
TGGAGTAACAGGCCCAGGGTTACAGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAACT  
CTGACCTCCGCAACAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCT  
CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCACCACTTCTACCTCGGCCCCAGTGAG  
ACCCACATCCACCACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAG  
AACACGAGGCCTCCCGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC  
CGCAGCAATTGAGGGCAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG  
TGTGGCTCCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTTACTGT  
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT  
CATCACTTCCTGTTCCCACTGACTGGGCTGGCCCAGCCCCTGTTTTTCCAACATTCCC  
CAGTATCCCCAGCTTCTGCTGCGCTGGTTTTCGGCTTTGGGAAATAAAATACCGTTGTATAT  
ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC  
TCCGCTTGTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTG  
AGAGAGAGGATGCTAAGCTTCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG  
GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGG  
GAATCGGTTCCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC  
CCAATTCGCCCTATAGTGAGTCGTA



**FIGURE 125**

MDPARKAGAQAMIWTAGWLLLLLLLLRGGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT  
EAVGAVETIHGQFSLAVRGCGSLPGKNDRGLDLHGLLAFIQQLQQCAQDRCAKLNLTSLAL  
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAAANVTV  
SLPVRGCVQDEFCTRQDGVTPGPGFTLSGCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT  
VASTTSVTTSTSAVRPTSTTKPMPAPTSQTPRQVEHEASRDEEPRLTGGAAGHQDRSNSG  
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

[illegible]

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**FIGURE 127**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK

CSFNQKPRAPGDDEEAQVENLITANATEPQKQORTEVQPSGGSLWNLRLLEPLDANVDA

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**FIGURE 128**

AAACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT  
CCTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG  
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT  
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAAGGAACTTCCTTT  
CCTCAACTGGGATGCCTTTCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT  
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT  
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCATCCAAA

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**FIGURE 129**

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE  
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

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**FIGURE 130**

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC  
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTC  
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC  
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT  
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA  
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT  
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATTATC  
TTCACTATTAATTGTAACGATTAAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT  
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA  
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT  
AAAAGTTTTGAGTATATTTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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**FIGURE 131**

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

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**FIGURE 132**

GGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG  
GCTGCTGTTGTTTCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA  
AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC  
TGCAGCTGCTACCATGGTGTTCATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG  
GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA  
GACTGTACCGGGAAAATGACTGCATGTTCCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT  
TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA  
GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC  
ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT  
CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCACAGTG  
GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG  
ATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTTGTTGATGCAGAATACACCAAAAAC  
CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT  
GGATCACTGCAAATACAAGTATCTGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA  
AACACCTCTTCCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCCTC  
TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCA  
AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA  
GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG  
AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT  
TCCCAAAATGTTGAAAACCTGAACCTATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCA  
ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA  
TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA  
AAGATTTAAAATGTGTCTAATACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA  
CCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCATTTTCTTAAGACCAATC  
ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA  
TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCATTTGGAAGTAGTACAA  
CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG  
AAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG  
TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTTACTCAG  
GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT  
TCAGGTTCCCTTTTTGTGCCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA



**FIGURE 133**

MEWWASSPLRLWLLLFLLP  
SAQGRQKESGSKWKVFIDQ  
INRSLENYEPCSSQNCSCYH  
GVIE  
EDLTPFRGGISRKMAEVVRR  
KLGTHYQITKNRLYREND  
CMFPSRCSGVEHFILEVIGR  
LPD  
MEMVINVRDYPQVPKWMEPA  
IPVFSFSKTSEYHDIMYP  
AWTFWEGGPAVWPYIPTGL  
GRWDL  
FREDLVRSAQWPWKKKNST  
AYFRGSRTSPERDPLILLS  
SRKNPKLVDAEYTKNQAWK  
SMKDT  
LGKPAAKDVHLVDHCKYK  
YLFNFRGVAASFRFKHLF  
LCGSLVFHVGDEWLEFFYP  
QLKPWVH  
YIPVKTDLSNVQELLQFV  
KANDDVAQEIAERGSQFIR  
NHLQMDDITCYWENLLSEY  
SKFLSY  
NVTRRKGYDQIIPKMLK  
TEL

**FIGURE 134**

CACCCCTCCATTTCTCGCC**ATG**CCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT  
TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT  
GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA  
CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC  
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG  
AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCC  
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGGCCACCTGGGTGCCGC  
TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT  
GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC  
TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCGCCACCCAGTGTGTG  
TGGAGCTGCTGACAGTGCTGTGGGTGGTGCCTACCCTGGGCACGGACCGTCTCCTCCTTGCT  
TTCCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT  
CCGGGCCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**  
**GAG**GAGCTCACTCTGGTTACAAGCCCTGTTCTTCCTCTCCCACTGAATTCTAAATCCTTAAC  
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT  
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA  
CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC  
TTCCTGTTTATAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC  
CTGACCACTCCCCTGGCACTGTTACTTGCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT  
GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA  
GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT  
GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC  
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

**FIGURE 135**

MAPALLLIPAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP  
LAWDLGLLLLFVGQHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV  
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP  
RALRLFSHLRHPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR  
KLHLLSRPQDGEAE

**Signal sequence:**

amino acids 1-13

**Transmembrane domains:**

amino acids 58-76, 99-113, 141-159, 203-222

**N-myristoylation sites:**

amino acids 37-43, 42-48, 229-235

**FIGURE 136**

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA  
 AGAAATTGCCAAACCATGTCTTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT  
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATT  
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA  
 TCACGTGGTGTCTCCGACTACTCACCCCGAGTGTAAGAACCCTTCGGCTCGCGTGCTTCTG  
 AGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCC  
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT  
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT  
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAATCCATTT  
 CTGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC  
 TTGGGGTGAAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG  
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCCTAGAGGATGAACACCTTCTTTATGGT  
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC  
 ATTCAGGTGGGTAACTGAGTTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG  
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT  
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATAT  
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAA  
 TGTCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAAACCCATCAAGTTT  
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAAAGTGAACATTCATATTCCAGAAGA  
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG  
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACC  
 ACATGCCATTATTAACTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA  
 GTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTTACACTG  
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTC  
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGTAAA  
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGG  
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTG  
 AACAAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA  
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT  
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAAATTA  
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT  
 CATTCTTTACATGCAAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC  
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTAAAT  
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

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**FIGURE 137**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD  
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK  
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTLKTIMAFRWVTEFCPNAKYVMKTDVDVFIN  
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPPYCSGLGYIMSRD  
LVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG  
FSSKEIITFWQVMLRNTTCHY

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**FIGURE 138**

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT  
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA  
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA  
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC  
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT  
TCAATCCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC  
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA  
AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC  
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT  
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT  
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT  
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

**FIGURE 139**

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS  
IWDYGNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQGKGPGGPPPKGLMYSVN  
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

**Signal Peptide:**

amino acids 1-20

**N-myristoylation Sites:**

amino acids 67-72, 118-123, 163-168

**Flavodoxin protein homology:**

amino acids 156-174

**FIGURE 140**

CATTTCTGAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA  
TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCG  
CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTCTTATTGCTTACTGATTTTTT  
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA  
GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG  
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT  
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT  
CAGATTCCGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT  
CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC  
TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA  
TTGAATCCGGATGGAACCTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC  
ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG  
TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAGAAAA  
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG  
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA  
GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT  
GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG  
TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG  
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT  
GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG  
CTGACTTTCTCTTCCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT  
ATGGACTCAATCAAAAACATTAAACGCAAACTGATTAGGATTTGATTTCTTGAAACCCTCTA  
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTTGCACATT  
AAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT  
TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTT  
ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT  
ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTTTACAAGGAAATAAAATACAAAT  
CTTGTTTTTTCTAAAAAAAAAAAAAAAAAAGT



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**FIGURE 141**

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY  
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEEK  
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN  
NRRSRSGTYSSRSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRSRSQ  
SKSRDHSDAAKKHRHERGHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHRR

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TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA  
TTTTTTGAANNTATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT  
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT  
CATATATAGGAAAATCGCATATGGTCCTAGTATTA AATTNTTATTGCTTACTGATTTTTTTTG  
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAAGA  
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGA ACTGGTTTGTTTACATGCA  
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT  
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA  
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC  
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAAGCCAACTATGAATTACTG  
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT  
GAATCCGGATGGA ACTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

**FIGURE 143**

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGTC**ATGGC**  
GGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC  
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTTTGTTCGGATACAAGCACCCG  
TCTGAGGAGGAGCTTCGGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG  
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG  
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGCTTCTTCCTGGAGTACCAGTGG  
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTCACAGAGGCCTACTACTACAT  
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT  
CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC  
TCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG  
GGAGGAGACCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC  
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAGCTGGCTATCCGCGTG  
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCCAGGCCTGCGGCTGGC  
CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCCTCCTGC  
ACACCAGCTTCCTGTCTCCCCTGTTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC  
TTCCTGCACCAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA  
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGCTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC  
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC  
CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT  
GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC  
TGGGAGGCTATTCTGGGGCCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC  
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG  
GGCCCTGGGTGGCCTGCTTACTCCCCTCTTCCTCCGTGGCGTCCTGGCCTACCTCATCTGGT  
GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA  
GGCTCC**TAG**CTGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA  
CTAGCCTGCCCCCTCTGTTTGCGCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC  
GGCGTTCCCTTCACCACAGTGCTGACCCGCGGCCCCCCTTGGACGCCGAGTTTCTGCCTCA  
GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCGAGGCCATTGTCTCCGAAGCGTATG  
TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC  
GATTTTTTAA

**FIGURE 144**

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEELRALAGKPRPRGRKE  
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY  
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLLAMLVQV  
VREETLELGLEPGLASMTQNLEPLLKKQGWDWALPVAKLAIRVGLAVVGSVLGAFLTFFPGLR  
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA  
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT  
VVSLOQYLTPLIILTNCTLLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVVQQTAAARI  
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLAS

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**FIGURE 145**

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC  
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT  
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC  
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC  
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC  
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT  
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT  
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTTCCTGACAGTGACACGGCTGTACTTCAGC  
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC  
CATGCTGGTGCAAGCG

**FIGURE 146**

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTT  
AATCTGAAGGTTCTCAGTCAAATTCCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC  
TTGGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGG  
CGCTTCTGTTGCTGGTCTTGCCTTGGCTCAGTCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTG  
TATTCAGAACTCTGTAAAGGTGCCCTCCCACTACGGCTGACCAAGATAGGAAGAGGCGCTCACAAGATGGCTG  
TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA  
TGACAGACGAGCCTGGCCTAGACAACCTGCCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCA  
GTGGACTCTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA  
AAAAATAAATCGAGCTTTGAGTGTCTTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGG  
GCAGGGAAAATTCTGAAAACACCCTGCCCTGAAGTCTTCCAAGGTTGTACCACCTGATTCAGATGGTGAA  
ATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC  
CCCCTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG  
GAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCCTGCGG  
CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGCAGCAGGAACAATGGACAGGCCCG  
GGATGCCTACAGACCCCGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGAA  
TAAACTGGTGCGCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA  
CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAGAAAG  
TGCGGCTCATCTGATTAGGCCAGTGAAAGACGTGTTACCTCGTCTGTCCCGCCAGGTTCCGCAGCGGAGCC  
CTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT  
CCCAAGCCCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCCGGTGAATCTCT  
CGGCATGACCGTTCGCAGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTGAGCCCG  
GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACTGACA  
GAGGTGAGCCGGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGT  
CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCA  
GTGACTGGTCCCCATCCTGGGTGATGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTA  
CGAAGAAACACAGCTGGGAAGTCTGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTT  
TTTCATCAAATCCATTGTTGAAGGAACACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTG  
CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA  
ATTACTCTAACTATTGTTTCTTGGCTGGCACTTTTTTATAGAAATCAATGATGGGTGAGAGGAAAACAGAAAAA  
TCACAAATAGGCTAAGGAAGTTGAAACACTATATTTATCTTGTGAGTTTTTATATTTAAAGAAAGAAATACATTGT  
AAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAATATGATTCCAAAAAATTA  
AACTACTAGTTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTACAACATTGTTTATATTTTTTCTATTCAAT  
AAAAAGCCCTAAAACAACATAAATGATTGATTTGTATACCCCACTGAATCAAGCTGATTTAAATTTAAATTT  
GGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTAAATTTACAGCTAAAATATTTTTTAAATGCA  
TTGCTGAGAAACGTTGCTTTCATCAAACAAGAATAAATATTTTTTCAGAAGTTAA

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**FIGURE 147**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDGCASLTAT  
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFFERSTIRSRS  
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP  
SELSIRLVGGSETPLVHIIIIQHIIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL  
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGV  
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQRS  
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE  
WDLPIYVISVEPGGVISRDRGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV  
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV  
GGYEEYNGNKPFFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI  
TLTIVSWPGTFL

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**FIGURE 148**

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT  
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGCTGACCATCT  
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC  
AATGTTTCAAGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC  
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC  
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT  
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG  
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCCTGCTTGGGTAC  
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT  
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG  
TGCAGACATTCATGTTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC  
TTGGTTTACTCTCAAAGTCAAATTAAATTCTTCCCAATGCCCCAACTAATTTTGAGATTC  
AGTCAGAAAATATAAATGCTGTATTTATA

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**FIGURE 149**

MKILVAFLVVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT  
IFDYKHGYIASRVLSRRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE  
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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## **FIGURE 150**

GGCACGAGCCAGGAAGTAGGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC  
**ATG**GGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG  
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTTCCCCAAAG  
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCCAGCCACCACCGCCCATCACCTATTCCCTC  
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT  
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT  
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG  
CCAGTGTCTGAGCTGCGGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA  
GATGATCTGCCAGGCGTCCTCGGGCAGCCCACCTATCACCAACAGCCTGATCGGGAAGGATG  
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG  
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC  
CCTCACAGTGGTGCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA  
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG  
GGGTTTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAAGCAGCAGCCATG**TAGA**ATGAACC  
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTTCGTATTTGGA  
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 151**

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAPQPPPPITYSL  
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMWELWSK  
PVSELNANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDGQVHLQQRPCHRQPANFSFLP  
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPIALPLYRSTRRLSEEEFG  
GFRIGNGEVRGRKAAAM

**Signal Peptide:**

amino acids 1-18

**N-glycosylation Sites:**

amino acids 86-89, 132-135, 181-184

**FIGURE 152**

GGTCCTTA**ATG**GCAGCAGCCGCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG  
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT  
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAGGCCAGGTGGATGAAAAGA  
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAAA  
CTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT  
TACAGAGCAACTGCGTGACATTAGCTGGAGAATTACACACCCAAGGAACCCCTCACCCCTGC  
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT  
TTCGATGGGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC  
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT  
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC  
CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACTCAGGGCCAC  
AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCA  
TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAG  
GTCTTGATCAAACTCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGT  
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCTT  
TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC  
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC  
TCTTTTGTGGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT  
GTCAGTAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG  
AATTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT  
TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

**FIGURE 153**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFL  
HYDCGNKTVTPVSPPLGKKLVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR  
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS  
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

**Important features:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 224-246

**N-glycosylation site.**

amino acids 68-72, 82-86

**N-myristoylation site.**

amino acids 200-206, 210-216

**Amidation site.**

amino acids 77-81

**FIGURE 154**

GGGAAAGCCATTTGCGAAAACCCATCTATACAAACTATATATTTTCATTTCTGCTGCTAGCTG  
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATAACCGTGGAATGGAG  
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG  
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA  
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC  
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT  
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAAC  
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCTGACATGCTCAACAGC  
ATTGCTTTTTTCCCCAAAATTAAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT  
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGCAGCAAGGGACC  
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTTCTGTAT  
CATCCTTTTCAATAAACTGTATTCATTTTGAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 155**

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA  
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

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**FIGURE 156**

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**  
 CTCTTGTGGCAGGTAACTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA  
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC  
 AGAACTGCCCCCTCCGTTTGCTCGTGCAGTAACCAGTTCAGCAAGGTGGTGTGCACGCGCCGG  
 GGCCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA  
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCAGT  
 TGGGCAGGAACTCCATCCGGCAGATTGAGGTGGGGGCCCTTCAACGGCCTGGCCAGCCTCAAC  
 ACCCTGGAGCTGTTCGACAACTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTC  
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCTCTTACGCCTTCA  
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT  
 GAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA  
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACT  
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTAG  
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACCT  
 CAACTTGGCCCCACAATAACCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC  
 TGGTGGAGTTGCATCTACACCACAACCCCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC  
 TGGTGGCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCCGCTGTCATGCTCCCAT  
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCT  
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT  
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC  
 CTCCCGCCACCCAAGGATCTCTGTCCTCAACGACGGCACCTTGAACCTTTTCCCACGTGCTGC  
 TTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG  
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTCACCACAGT  
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTTA  
 CCACGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTTCAGACTACC  
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT  
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG  
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGCGGAGTACAGTC  
 ACAGCCGCCCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGC  
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATTC  
 ATGACCATATTAATACTACAACACCTACAAACCAGCACATGGGGGCCACTGGACAGAAAACAGC  
 CTGGGGAACTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTTCAGACCCA  
 TACCAAGGACAAGGTACAGGAACTCAAATAT**TGA**CTCCCCCTCCCCCAAAAACTTATAAAAT  
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA  
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAACAGATTATATTAATAATTAAAGA  
 CAAAAAGTCAAAACA



**FIGURE 157**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT  
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS  
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY  
ISEGAFEGFLNLKYLNLGMCNIKDMPNLTPLVGLEELEMGNHFPFPEIRPGSFHGLSSLKKLW  
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHNPWNCDILW  
LAWWLREYIPTNSTCCGRCHAPMHRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL  
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN  
ASAYLNVSTAE LN TSNYSFFT TTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ  
TTRVPKQVAVPATDTTDMQTSLEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLKRHQQRS  
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE  
NSLGNSLHPTVTTISEPYIIQTHTKDKVQETQI

**FIGURE 158**

CGCTCGGGCACCAGCCGCGCAAGGATGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCC  
TTCTCATCTCGTCCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATG  
TGTCGGGAGTGCTGTGAATATGATCAGATTGAGTGCGTCTGCCCCGAAAGAGGGAAGTCGTGGGTTATACCAT  
CCCTTGCTGCAGGAATGAGGAGAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAAC  
GCAAGAGCTGCCGAAATGGCTCATGGGGGGGTACCTTGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAG  
TGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGTCAGATTTT  
GTTGGAAAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTTCATGCTAAACCTGGGTTTGTATCCAACTAA  
GATTTGTATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTCGTGATGGAGACAAC  
CGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACT  
CCACGTCCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCAT  
GCTCCTCATCCCCTTGTTTCCATGACGGCACGTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCCTGCTTG  
GCAGGCTATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCCTGGGGGGCCAGTCAA  
TGGGTACCAGAAAATAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTGGCACCCTGGTGTCTT  
TCTTTTGTAACTCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGG  
AAACAGCCCCTCTGCATAAAAGCCTGCCGAGAACCAGATTTCAGACCTGGTGAGAAGGAGAGTTCTTCCGAT  
GCAGGTTCACTCAAGGGAGACACCATTACACCAGCTATACTCAGCGGCCTTCAGCAAGCAGAACTGCAGAGTG  
CCCCTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAG  
TATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAG  
TGGGCGGGCACCATCCTGCATCCTATCTGCGGGAAAATTGAGAACATCACTGCTCCAAAGACCCAAAGGTTGC  
GCTGGCCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCCTACACAAGGGAGCGTGG  
TTCCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGG  
GAAGGTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGGAAATTCTACCGGGATGATGACCGGGATG  
AGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTCTGCATCCCAACTATGACCCCATCCTGCTTGATGCT  
GACATCGCCATCCTGAAGCTCCTAGACAAGGCCCCGATCAGCACCCGAGTCCAGCCCCTGCTCGCTGCCAG  
TCGGGATCTCAGCACTTCCTTCCAGGAGTCCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGACGTGAGGA  
GCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACTCGTGCTGTGTGAGGAGCAG  
CATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCCCTC  
TGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGTCTTCCCGGACGAGCATCTCCTGAGCCACGCT  
GGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCACTGCCTTCACCAAG  
GTGCTGCCTTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAGTGTTC  
TGTATATCCGTCTGTACGTGTGTATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTTGGCCTGTGAACCTGG  
CTGTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGAT  
GCCGCTCCACTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAAGAAGACC  
ATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCCAACTTTTCACTTATACGAATGCCATCAGCTTG  
ACCAGGGAAGATCTGGGCTTCATGAGGCCCTTTTGAGGCTCTCAAGTCTAGAGAGCTGCCTGTGGGACAGCC  
CAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTTTGTGTACATGGCCACAGTACAGTCTGGTCCCTTTCTTCC  
CCATCTCTTGTACACATTTTAAATAAAATAAGGGTTGGCTTCTGAACTACAAAAAAAAAAAAAAAAAAAAAA  
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AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 159**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV  
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD  
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD  
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG  
TCVLDKAGSYKCACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV  
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLH  
QLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK  
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE  
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD  
ADIAILKLLDKARISTRVQPICLAASRDLSTS FQESHITVAGWNVLADVRSPGFKNLTLRSG  
VVSVDSSLCEEQHEDHGI PVSVDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR  
WHLMGLVSWSYDKTCSHRLSTAFTKVL PFKDWIERNMK

**FIGURE 160**

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA  
AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC  
TTCAACCTGACTTTCCACCTTTCCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCT  
GACAGTGGTTGGGTGGGCCACCAGTAACACTTCTGTTGGGTGCCATTCAAGAGATTCTTAAAG  
CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT  
AATGAAGCATCCACGAAGAAGGTAGAAGTTGACAAGTGTCTTCTGTGTCTCCTTACCTCAG  
AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC  
CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC  
CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT  
CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT  
TTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC  
TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA  
GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG  
GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT  
AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG  
AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG  
ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCACGAGTCTGG  
AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA  
TATCAACATCACAGTGGATTTCTGGTTTGGTGCATGACGACCCTGGATCTTTTGGTGATGTTTGG  
AAGAACTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA  
AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTTGTATTTTCTTAGCAGAGCT  
CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG  
AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT  
AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT  
TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT  
CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTTCATTTATCCTGTACAATCATCT  
GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA  
GGACACAGTGAAGTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG  
CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCCAGGTATGCCT  
TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAATAATGA  
TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAATA  
TGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAGCAAAA

**FIGURE 161**

MGFNLT FHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT  
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV  
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKGKFNRAKLLNVGYLEALKEEN  
WDCFIFHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSYFGGVTALSREQFFKVNG  
FSNNYWGWGGEDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR  
VWRDGLSSCSYKLVSV EHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites:**

amino acids 4-7, 220-223 and 335-338

**Xylose isomerase proteins:**

amino acids 191-201

**FIGURE 162**

CGTGGGCCGGGGTTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGCAGTTCTC  
GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCCGCA**ATG**  
GCCCAGGCAGTGTGGTCGCGCCTCGGCCGCATCCTCTGGCTTGCTGCCTCCTGCCCTGGGC  
CCCGGCAGGGGTGGCCGCAGGCCTGTATGAACTCAATCTCACCACCGATAGCCCTGCCACCA  
CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG  
CCCGCTGACGCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA  
GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTTCGGCCACGTGCCCCGGGAATTCCCGG  
TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG  
GTCCTCCCCATCACAGAGTTCTCGTGGGGGACCTTGTTGTACCCAGAACACTTCCCTACC  
CTGGCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCCCTCCTCCACGACCCGA  
GCAACTTCTCAAGACCGCCTTGTTTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG  
GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCT  
CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA  
CCGGGGACTTCTCCGCCTCGCTGAAGCTGCAGGAAACCCCTTCGAGGCATCCAAGTGTGGGG  
CCCACCCTAATTACAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTGGGGAGCCCTCC  
TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCTCCCGCTGGAGGAAGGGGAGTGCCACC  
CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTGGGGACTAC  
TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT  
GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA  
TGTTGGCCTTCATCATGTACATGACCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG  
AACCCGGAGCCACCCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCCTTTCTTGCT  
GGAGACTCCATCTGAGTACCTGGAAATTGTTCTGTGAGAACCACGGGCTGCTCCCGCCCTCT  
ATAAGTCTGTCAAACTTACACCGTGT**AG**AGCACTCCCCCTCCCCACCCCATCTCAGTGTAA  
CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCATT  
TGGCTGGGGCTGTGGCCTGGATCATCCATCCATCTGTACAGTTCAGCCACTGCCACAAGCC  
CCTCCCTCTCTGTACCCCTGACCCCAAGCCATTACCCATCTGTACAGTCCAGCCACTGACA  
TAAGCCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT  
TTGATGCTTGGGGTGTTCGTGTGACTCCTAGGTGGGCCTGGCTGCCCACTGCCCATTCCT  
CTCATATTGGCACATCTGCTGTCCATTGGGGGTTCCTCAGTTTCCCTCCCCCAGACAGCCCTAC  
CTGTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC  
ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACACACACACACACA  
CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTTCAGATGATCAGCTCTGTA  
TCTGGTTAAGTCGGTTGCTGGGATGCACCTGCACTAGAGCTGAAAGGAAATTTGACCTCCA  
AGCAGCCCTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCAGTTCTTGC  
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCCTGGATGGGGGGCAGGACT  
AATACTGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTG  
AACTTTCACTGAGGAAAAGGCCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGG  
TGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA  
GATCGAGACCACCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAAGTT  
AGCCGGGCGTGGTGGTGGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG  
GTGCGAACCCGGGAGGCGGAGCTTGCAGTGAGCCCAGATGGCGCCACTGCACTCCAGCCTGA  
GTGACAGAGCGAGACTCTGTCTCCA

**FIGURE 163**

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA  
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF  
VVLPITEFLVGDLVVTQNTSLPWSSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ  
MVTEDSVVYYNYSIIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL  
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD  
YCFIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV  
ENPEPPSGVRCCCQMC CGPFLLET PSEYLEIVRENHGLLPPLYKSVKTYTV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 339-362

**N-glycosylation sites.**

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

**FIGURE 164**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT  
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA  
CAACAGACGGGACAACCTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG  
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCT  
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAGA**ACCTACCTGCCCTG  
CCCCCGTCCCCTCCCTTCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA  
TGGCTGGTTCTTTTGTTCACAAA  
AA

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT



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**FIGURE 165**

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRDTH  
FPICIFCCGCCHRSKCGMCCKT

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CTGTACAGGAAGGACCATCTGAAGGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC  
CTGGATCTTCCACC**ATG**TTTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC  
ATCTCCCTGACTGTCCTCTTCACCCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTTGG  
AGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA  
CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC  
GGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGG  
TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC  
GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG  
GAGTCCTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC  
GGTCTGTGTTTTGGGTTAGGAGTGCTGATTCTGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC  
TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT  
GGGAGGTTTAAGGAATTTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG  
AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT  
GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGCCAGCGATGGCTATTATGCC  
ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTGAGAGAGCCATGGTGAAGGCCTG  
CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA  
CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCCAGAAGGAACCTGCATC  
ATAATACATCGGTGATGATGTTCAAAAAGGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC  
TGTTGCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGA  
TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG  
CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC  
CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCTGAAGAGGGGAGAAGG  
TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCCAC  
AAGGACAGGAGCCGCTCCT**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA  
CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCCACTGCTGTGTCTTTCCAGACTCCAGGG  
CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGCAGCGGGATCCCTGT  
GCACCCGGCGCAGCCTACCCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA  
CGAGATGCCTTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCCA  
CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT  
GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG  
CTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGC  
CTTGGAGCTCTGCAGACATGATAGGAAGGAAACTGTCACTCTGCAGGGGCTTTCAGCAAAATG  
AAGGGTTAGATTTTTTATGCTGCTGCTGATGGGGTTACTAAAGGAGGGGAAGAGGCCAGGTG  
GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTGCTCGTACTCCAGGCTAACCTGAACTCCCC  
ATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG  
GAATGGTGGTGATTTCCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGA  
AGGACACATCACGTTCAGTGTTTTCAAGTACAGGCCACAAAACGGGGCACGGCAGGCCTGAG  
CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAAACTGGCTGGTGAA  
TGA

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**FIGURE 167**

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIIVPAIFGVSEFGIRKLYMKSLLKIFAWATLRME  
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRSKGSSKALDNTPEFELSDIFYFCRKGME  
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLPLRIALAFTG  
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH  
TSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ  
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL  
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF  
KEEQQKLYSKMIVGNHKDRSRS

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**FIGURE 168**

GCCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA  
CGTCTCCTCCAGGGATGGCCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC  
ACCTGGCAGGCCCAGGCTGTTCCCACCATCCTGCCCCTGGGCCTGGCTCCAGACACCTTTGA  
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG  
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC  
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT  
CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG  
GCTCCCGGGAGCTCTACATGAGGCACTTTCCTTCAAGGCCCTGCATTTCTACCTGATCCGG  
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG  
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT  
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTGGGGAGAAGAGGCGGGGCTGT  
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG  
GAAGACTCTGCTCTTGGCCCCTGGAGAGTTCCAGCTCTCAGGGGTTGGGCCCTGAAAAGTCCA  
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG  
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACCAGG  
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTGCTATGTGATGGGGACTTCCT  
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA  
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

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**FIGURE 169**

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH  
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSREL  
YMRHFPPFKALHFYLIRALQLLRSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS  
LDKAVAHREFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLLAPGEFQLSGVGP

GTGGCTTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA  
CCCTCATCTATATCCTTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG  
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC  
TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCA  
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG  
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT  
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG  
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG  
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC  
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT  
GCGTTGCCAGGAACCCTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT  
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCCCT  
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG  
AGTACATTGAAGAGAAGAAGAGAGTGACATTTGTGGGAAACTCCTAACATATGCCCCCAT  
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA  
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCAC  
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTTAGACAGCAGTG  
CACTCCCCTAAGTCTCTGCTCA

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**FIGURE 171**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT  
IQPEGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV  
YEHLSPKPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW  
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW  
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP  
KKMENPHSLLTMPDTPRLFAYENVI

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**FIGURE 172**

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC  
TCTGGACCCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC  
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC  
AGCCAGAAGGGGGCCTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA  
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT  
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG  
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG  
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT  
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG  
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAACTTCTCAAGCCCC  
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCT  
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC  
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA  
ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA  
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAA  
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAG  
AATGTTATCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 173**

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAA**ATG**AAGATGCTGCTGCT  
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA  
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA  
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA  
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG  
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT  
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA  
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA  
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT  
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC  
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC  
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC  
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT  
TTTTCATGAAATTATTCCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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**FIGURE 174**

MKMLLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ  
IHVLENSLVLVKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI  
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA  
TGGATTACAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG  
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC  
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG  
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA  
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC  
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA  
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG  
GTTTTCAATAAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTTCCAC  
TTCGATTCTGAAGAAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT  
TGTTGGAATTCTGGAGGTCTGTGTTGGGCTCAGTCAGATAGTCATCGGTTTTCTTGCTGTC  
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA  
TCAGTAGTTTTGAAAAAAAAAAAA

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**FIGURE 176**

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA  
IPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNA  
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL  
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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**FIGURE 177**

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT  
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT  
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC  
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTG  
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAA**ATAG**TGAA  
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC  
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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**FIGURE 178**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV  
KHCTDQISFKKRLSLKKSWWK

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**FIGURE 179**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG  
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG  
GAGCAGATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTC  
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG  
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG  
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG  
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC  
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA  
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC  
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG  
CCCCACCACCCCCTCA

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**FIGURE 180**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK  
YKSSQKQHSPVPEKAIPITPGSATTC



GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCCC  
TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC  
CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACTGCCGCCGGCTCC  
AGTGTTTCCACAGCCCCCAAACGGAACTGGTTTTGGGGTACCTGGGCCTGATCACTCCT  
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGT  
ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTTATGCCACCCTGACACCATCCGGTCTATCA  
CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG  
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC  
GCCCCGCTTCCATTTCAACATCCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACA  
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGGCAGCAGTCGTCTGGACATGTTTTGAG  
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG  
TCAGGAGAGGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTTAGAGAAAA  
GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGGCGC  
TTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTTCATCCGGGAGCGGCGTGC  
CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG  
ATTTCATTTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT  
ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC  
CTGGGTCCCTGTACAACCTTGCGAGGACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC  
AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCC  
TTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCCG  
ATGCTGCACCCAGGACATTGTTCTCCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC  
TCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGAC  
CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCTTTCTC  
CGCAGGGCCCAGGAACTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCCTGG  
CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAA  
TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCA  
GT**G**ACTTTTCTGACCCATCCACCTGTTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

**FIGURE 182**

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG  
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF  
IRFLKPWLGE GILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQH LASEGS  
SRLDMFEHISLMTLDSLQKCIFSFD SHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY  
LSHDGRRFHRACRLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDG  
KALSDEDI RAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW  
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW  
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT  
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

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**FIGURE 183**

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC  
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA  
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA  
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG  
AAAGCAGACTCAAGTACCAACATTTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT  
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA  
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTCTTGAAGTGAAATAAGCATCTGT  
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAAC  
AGTGTGGAGAAAAACTAGGCAAACTACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT  
ATGTTTTGCACAAAAAAAAAAAAAAAA

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**FIGURE 184**

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA  
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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**FIGURE 185**

GAACATTTT TAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT  
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA  
CCACCTCCGCCAGGAACTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC  
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT  
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA  
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA  
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT  
CAGGGGTT CAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG  
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGCCTTACTCACCTCTCTCT  
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA  
CAAGCTCAGGAGGCGAATAAATGTTCAAACCTGTA

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**FIGURE 186**

MPSPGTVCSELLLGLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG  
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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**FIGURE 187**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC  
GTGAACCCCGGGGTGCTCCGCACGGACCCCAGATGTCAAGAAT**ATGA**ACACGTGGCTGCTGT  
TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG  
CTCCTGCTGGACTTTCTTGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT  
GAGTATGTCCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC  
TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT  
GTCCCCCGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCAGAAAGTGAGATCATGGACAAAAA  
GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC  
TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCT**TGA**AGTAACAAGTTTAAAATGTTCAGA  
GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT  
CCAAAAACACAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTCACCCCTAACCA  
AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC  
AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT  
AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTGGTCATGGTGGGCCAGCTGCAAAGCG  
TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC  
ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA  
ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA  
GCATCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCACCAAGA  
GCCTCCTTGTTCATAACCACAGGTTACCCTACAAACCACTGTCCCCACACAACCTGGGGAT  
GTTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA  
ATTTTTTTTAAATGAAAGTGCAATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 188**

MNTWLLFLPLFPVQVQTLIVVVIIGMLVLLLDLGLVHLGQLLIFHIYLSMSPTLSPRSPQGW  
VVRAAHLTPLEYYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ  
AQQEAEELTPRPAGVPGA

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**FIGURE 189**

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG  
ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT  
ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG  
TGCCCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG  
GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGGGAGACTGGGGATGA  
CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG  
AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAA  
GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAA  
GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA  
TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT  
ACTAACAGACTTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG  
CTGTTTCTCTGTCTGTGCTCAGGTCTCCTGGGGATGGTGGCCCACATGATGTATTACAAAGTC  
TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAATTATGGCTG  
GGCCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCACCACCTTCA  
ACACGTACACCAGGATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAAC  
CCGAACCTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCCAC  
CGTGGGTCCCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG  
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG  
AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA  
GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG  
TCTCTTGAGCATGGTTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC  
CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCAC  
CCCACATCTCACACATCCAGAATTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC  
TAAACCATGGAGATAAAAAGAAGAGTAAATACTTCCCCGACCTTAAGGATCTGAAA

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**FIGURE 190**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP  
VSLDGD TNTSTQEVVQYNWETGDDRF SFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR  
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL  
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLTTCLE  
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

**FIGURE 191**

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTG  
TCTTTATGTCTTTCTCCTCTTCCTATTCTGTGCATCTCCCTCACTTAAGTCTCAGGCCTGTCA  
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG  
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT  
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG  
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCCTCCCAA  
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAAG  
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT  
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCCTTCCCCCTGCCCCGCCGTAGATTGAG  
GACATTCGCCCCCTGTGTGCCACCAAACCAGGACTTCCCCCTTGGCTTGGCATCCCTGGCTCT  
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT  
ATGGCGATGGCCATGATGTTACAATCCCACCTGCCTGAATAATCAAGTGGGAAGGGGAAGCA  
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAAA  
GGGAAGCAACAGGAACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC  
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA  
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG  
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG  
AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC  
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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**FIGURE 192**

MWLPLGLLSLCLSPILSSPSLKSQACQQLWTLPSPLVAFRANRTTYVMDVSTNQSGME  
HRNHLCFCDLYDRATSPPLKCSLL

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**FIGURE 193**

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGGAGCCAGGAGCGACGTCA  
CCGCC**ATG**GCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTT  
GGATGTGCCCTTCCAATATACAACAAATACTGGCCCTCTTTGTTCTATTTTTTTACATCCTTTCACCTATTCC  
ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAACCTGCCATCTTTC  
TTACAACGGGCATTGTCGTGTGAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGGA  
GCTTGTGCACTTGTCTCACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTTCTTGGTCTTTGGAAG  
CAATGACGACTTCAGCTGGCAGCAGTGGT**G**AAAAGAAATTACTGAACATATTGTCAAATGGACTTCCTGTCAATTT  
GTTGGCCATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTA  
GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTTCACAGAGACTTGCTGAAGGATTAAAGGATTTTCT  
CTTTTGGAAAAGCTTGACTGATTTTCACTTTATCTATAGTATGCTTTTTGTGGTGTCTGCTGAATTTAAATAT  
TTATGTGTTTTTCTGTTAGGTTGATTTTTTTTTGGAATCAATATGCAATGTTAAACACTTTTTTAAATGTAATCA  
TTTGCATTGGTTAGGAATTCAGAATTCGCCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATTTATT  
TAGCCTCCATTATTACAAAAAATTATAAAAAAAGTTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG  
CAGACATACAGACGGTTGGCATACTGTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG  
GGGCAAGTGTTAATGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG  
AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGAATTTATGTTAAACTTTA  
AGGTAAGGGTGTA AAAACATTTTTGAGATAAGGTTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGT  
GGGAAGAAATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAAATTTGTGATCTCCTATC  
AACCTTTTCATGTTTTACCCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGC  
ATCATATATGCCAGAAAACCTTCTCTGCTTCTCTCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAA  
TAACTTTTCAAATATAGTTTAATAACACTTAGAAGTGTTTACTTACCTGGAAAATAAATTGCTATGCCGTACATT  
CAGAGTGCCCCCTCCCCTGCAAGGCCTTGCCATGATTAACAAGTAACCTGTTAGTCTTACAGATAATTTCATGCA  
TTAACAGTTTAAAGATTTAGACCATGGTAATAGTAGTTCCTTATTCTCTAAGGTTATATCATATGTAATTTAAAG  
TATTTTTTAAGACAAGTTTCTGTATACCTCTGAAGTGTGTTTATTTGAGTTTCATCATGATAGATCTGCTGTTT  
CCTTATAAAAGGCATTTGTTGTGTGAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT  
ACCTGACCAAAAAAATTCAGTAACAGGCATGATCAATTTATAGTGGTCTGTTTACATCTAATAATTATCAGGA  
CTTTTTTTCAGGAGTGGGTTATAAAAAACATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTTGTATG  
TTTATTTCAGTATACTTACATAAAAAATTATTTGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGT  
TTTATGAAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTTGTTTCAGCTTTTTTACTAAAGATGCCTAA  
AGCCACAGGTTTTATTGCCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG  
GCGTGTGGCTGGAGCCTTCCCCTGGAGGCTGAAAGTGGCTTGTGGTATTATAATGTTTCAGATTTCAAGAGGAA  
GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTGTGCTTGTGATCTACTGGACTTT  
TTTTTTGCAAGGAAGTGCAATCTCTGGTCTTCCCTATTTTCTGTTCTGGATGTCAGTGCAGTGCAGTGCCTACTG  
TTTTATCCACTTGGCCACAGACTTTTTCTAACAGCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCATT  
GTGTCTTTGACCTTGTATACTAGCTTGACATAGTGCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT  
TTTCCATAGAATATGCACTGATACAACATTACCATTCTTCTATGGAAAGAAAACTTTTGATGATGAAACAATAA  
AGATTTTAAATATCTATTTTAAAAA

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**FIGURE 194**

MAGIKALISLSFGBAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM  
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGCALVLTGNTVIFATILGFFLVFGSND  
DFSWQQW

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[illegible]

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH  
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQ  
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS  
LKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRILISLHSLCLRRNKVAIV  
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT  
LAGNLWDCGRNVICALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSG  
HLLSAVTNRSDLGPPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA  
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH  
IEGALVIINEYGSCTCHQQPARECEV

[illegible]



GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCCGGGTCCTGCTGTGGCTGCAGCTCTGC  
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTGCGAGCCAA  
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGGCGCCGTTGAGTTCCCGGCGGACAAGATGG  
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA  
CTCGTCCTGGCTTCAGGAGCCGGATTCTGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG  
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT  
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC  
CACGACGACGTCTTCTTTCCGCCTAGTGCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG  
CCCCGTGCGTGTC CGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG  
CTGTTTTCTGGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGCCGGGCGCGC**TGA**GCGTG  
GGCCCCGAGGACTGCGCGGACCCGTCGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG  
GATCTGCGCGGCCCTGCTCCAGCCCCCT

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**FIGURE 198**

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE  
GHAUSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA  
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVRVRSISALGRTFTRDEDLAVFLASR  
AGRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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[illegible]

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**FIGURE 200**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP  
FARDAVKKCFVCLA

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TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCTCCAGTACACCTCCCGCCGTTACCCGCGGGCGCG  
CCGAGGGAGTCTCCTCCAGACCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT  
GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACTACCATCCATAGCCAGATAGATTATCTTACACTG  
AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTGTCTTTCATACTTTGCTGCACTGAGTCTTTT  
AACCACCTTTTCTCTCCAATAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACT  
TATATAAGTTTCCAACGCCCCATTTTCATTATATTATGAATATGGTGTTCCAGTGAAGCAAGTTACTAATGTT  
TTTATTACAAAAACCTTACCCTAACCATTTATACTTTTGGTAAGTGGCCTCTTTGCAGAGAATCATGGGATTGTTGC  
AAATGATATGTTTGATCCTATTCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCCAAGTTT  
GGGAAGAAGCGACACCAATATGGATCACAAACCAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGA  
ACAGATGTA AAAATACATAAGCGCTTTCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG  
AGTTGCCAAAAATTGTTGAATGGTTTACGTCAAAAGAGCCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTT  
ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCAATTCAGATATTGACAAGAAGTTA  
GGATATCTCATACAAATGCTGAAAAAGGCAAGTTGTGGCAACACTCTGAACCTAATCATCACAAGTGATCATGG  
AATGACGCAGTGCTCTGAGGAAAAGGTTAATAGAACTTGACCAGTACCTGGATAAAGACCACTATAACCTGATTG  
ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAGGTAAATTTGATGAAGTCTATGAAGCACTAACTCACGCT  
CATCCTAATCTTACTGTTTACAAAAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTC  
ACCAATCATAGCAGTGGCTGATGAAGGGTGGCATTCTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACC  
ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTACCCCATGGTCTGCTTGCCTTCAGAAAGAATTT  
TCAAAAAGAGCCATGAACCTCCACAGATTTGTATCCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA  
CAATGGATCATTTCTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA  
CTATACTCCTCCTGGTAGTGTTAAACCAGCAGAATATGACCAAGAGGGGTATACCCTTATTTTCATAGGGGTC  
TCTCTTGGCAGCATTATAGTGATTGTATTTTTTGTAAATTTTCATTAAGCATTTAATTCACAGTCAAAATACCTGC  
CTTACAAGATATGCATGCTGAAATAGCTCAACCATTAATACAAGCCTTAATGTTACTTTGAAGTGGATTGTCATA  
TTGAAGTGGAGATCCATAATTATGTCAGTGTTTAAAGGTTTCAAATCTGGGAACCAGTCCAAACATCTGC  
AGGAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACATACACACACACGACCAA  
ATACCTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGTCTCCATTGTTCACTGTAGCATAGGGATAGATAAG  
ATCCTGCTTTTATTTGGACTTGGCGCAGATAATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATAT  
ATTGCACTTTAAATTTCTCTCCTGATGGGTACTTTAATTTGAAATGCACCTTATGGCAAGTTATGTCTTATAAC  
TTGATTGTAAGTGAACAATTTTTCACCCATGTACAGATAACTTGTACGCATTGTTCAAGTGAAGGAATTT  
TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCATAAATTTGAGAGAAGAAGAAGGTGATAAGTGTGA  
AAATTAATGTGATAACCTTTGAACCTTTGAATTTTGGAGATGTATCCCAACAGCAGAATGCAACTGTGGGCAT  
TTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTCATTTATTTTTCCCTCAAAGAGAGTCAAATACTGACAG  
ATTCTGTTCTAATAATATTGTTTCTGTCAAAAAATATTGTGATTTTCTGATGAGTCATATTACTGTGATTTTCA  
TAATAATGAAGACACCATGAATATACTTTTCTTCTATATAGTTTCAAGCAATGGCCTGAATAGAAGCAACCAGGCA  
CCATCTCAGCAATGTTTTCTCTTGTGTAATTTTGTCTCCTTTGAAATTAATCACTATTAAATTACATTAA  
AAATCAAATTTGGATAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 202**

MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK  
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIW  
ITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY  
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER  
LIELDQYLDKDHYTLDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN  
SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD  
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF  
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

**FIGURE 203**

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAGTGCAGGAGGCCAG  
GACAGGCCCCACCCTGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGC  
AGAGAGGCCAAGCCCCCTTGCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA  
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC  
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA  
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG  
AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCC  
CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT  
CAGCTCCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC  
TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCCGACAAGAATAACTATGCTGCCATG  
GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT  
ATTTGTCTTCCGCCTGAGTTCCTTACCACAAAGTTTGAGATCCTGGATGCCCCTCGTGGTGG  
TGGTCTCATTCATCCTGGACATTGTCCTCCTGTTCCAGGAGCACCAAGTTTGAGGCTCTGGGC  
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT  
TAAGACACGTTTCAGAACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA  
AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCTGGACTGATGAGTTTGCTGTATC  
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT  
CACACAGCCACCGTGAAAGTCCTGGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG  
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA  
TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC  
AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 204**

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEEEQPPPTPV  
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILDL  
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILDI  
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRLKQMNVLAAKIQHLEFS  
CSEKPLD

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CGCTCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGACCCAGCAGGCCGCCAACAT  
**G**CTCTGTCTGTGCCTGACGTGCCGGTCATCGGGGAAGCCCAGACCGAGTTCCAGTACTTTG  
AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCCCTCC  
CAGGAATTCTCCACCTACCGCCAGTGGAAAGCAGAAAATTGTACAAGCTGGAGATAAGGACCT  
TGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGA  
GGCTGGTGTTTAAGATTTTGGACAAAAGAATGATGGACGCATTGACGCGAGGAGATCATG  
CAGTCCCTCGGGACTTGGGAGTCAAGATATCTGAACAGCAGGCAGAGAAAAAATTCTCAAGAG  
CATGGATAAAAAACGGCACGATGACCATCGACTGGAACGAGTGGAGAGACTACCACCTCCTCC  
ACCCCGTGGAAAACATCCCCGAGATCATCCTCTACTGGAAGCATTCACGATCTTTGATGTG  
GGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGGGGATGTGGTG  
GAGACACCTTGGTGGCAGGAGGTGGGGCAGGGCCGTATCCAGAACCTGCACGGCCCCCTGG  
ACAGGCTCAAGGTGCTCATGCAGGTCCATGCCTCCCGCAGCAACAACATGGGCATCGTTGGT  
GGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGGTCACCTCTGGCGGGGCAATGGCATCAA  
CGTCTCATAAATTGCCCCGAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC  
TTGTTGGTAGTGACCAGGAGACTCTGAGGATTCACGAGAGGGCTTGTGGCAGGGTCTTGGCA  
GGGGCCATCGCCACGAGCAGCATCTACCCAAATGGAGGTCCTGAAGACCCGGATGGCGCTGCG  
GAAGACAGGCCAGTAGTCAGGAATGCTGGACTCGCCAGGAGGATCTGGCCAGAGAGGGGG  
TGGCCGCTTCTACAAAGGCTATGTCCCAACATGCTGGGCATCATCCCCCTATGCCGGCATC  
GACCTTGCAGTCTACGAGACGCTCAAGAATGCCTGGCTGCAGCACTATGCAGTGAACAGCGC  
GGACCCCGGCGTGTGTGCTCCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGG  
CCAGCTACCCCCCTGGCCCTAGTCAGGACCCGGATGCAGGCACAAGCCTCTATTGAGGGCGT  
CCGGAGGTGACCATGAGCAGCCTCTTCAAACATATCCTGCGGACCAGGGGGCTTCGGGCT  
GTACAGGGGGCTGGCCCCCAACTTTCATGAAGGTTCATCCAGCTGTGAGCATCAGCTACGTGG  
TCTACGAGAACCTGAAGATCACCTTGGGCGTGCAGTTCGCGGTGACGGGGGAGGGCCGCCCG  
GCAGTGGACTCGCTGATCCTGGGCCCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATG  
TGCCAACACTAAGCTGTCTCGAGCCAAAGCTGTGAAAACCCCTAGACGCACCCGCAGGGAGGGT  
GGGGAGAGCTGGCAGGCCACGGGCTGTCTGCTGACCCAGCAGACCCCTCTGTTGGTTCC  
AGCGAAGACCACAGGCATTCCTTAGGGTCCAGGGTCAGCAGGCTCCGGGCTCACATGTGTAA  
GGACAGGACATTTTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGCTTAGT  
TCTTCCATTTACCCCTTGCAGCCAGCTGTTGGCCACGGCCCCCTGCCCTCTGGTCTGCCGTGC  
ATCTCCCTGTGCCCTCTTGCTGCCTGCCCTGTCTGAGGTAAGGTGGGAGGGAGGGCTACAG  
CCCACATCCCACCCCCCTCGTCCAATCCCATATCCATGATGAAGGTGAGGTACGTTGGCCT  
CCAGGCTGACTTCCCAACCTACAGCATTGACGCCAACTTGGCTGTGAAGGAAGAGGAAAG  
GATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT  
TGGGAGTGCAGGGGGCTCGGGCTGCCTGGCCTGGCTGCACAGAAGGCAAGTGCTGGGGCTCA  
TGGTGCTCTGAGCTGGCCTGGACCCCTGTCAAGATGGGCCCCACCTCAGAACCACAACTCACTG  
TCCCCACTGTGGCATGAGGGCAGTGGAGCACCATGTTTGAAGGCGAAGGGCAGAGCGTTTGT  
GTGTTCTGGGGAGGGAAGGAAAAGGTGTTGGAGGCCTTAATTATGGAATGTTGGGAAAAGGG  
TTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG  
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTTCTGTCCAACC  
CCAGCAGGGGGCGCAGCGGGACCACCCACATTCACCTTGTGTCACTGCTTGGAAACCTATTT  
ATTTTGTATTTATTTGAACAGAGTTATGTCTTAATTTTATAGATTTGTTTAAATTAATA  
GCTTGTCACTTTCAAGTTTCATTTTTTATTTCATATTATGTTTCATGGTTGATTGTACTCTCC  
AAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCCCTTGGGCCGCTGCAGTCACAT  
CTGTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAGGCAGCAGCCCTG  
GCTCCTTTTCTTTTGGCAGGTTGGGGAAGGGCTTGGCCCCAGCCTTAGGATTTCAAGGGTTTGA  
CTGGGGGGCGTGGAGAGAGAGGGGAGGAACCTCAATAACCTTGAAGGTGGAATCAGTTATTT  
CTGCGCTCGAGGGGTTTCTTATTTCACTCTTTTCTGAATGTCAAGGCAGTGAGGTGCCTCT  
CACTGTGAATTTGTGGTGGGGCGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCCGTCCCTCC  
CAGCCTTCTGCTGCCCTTGCTTAACAATGCCGGCCAACTGGCGACCTCACGGTTGCACTTCC  
ATTCCACCAGAATGACCTGATGAGGAAATCTTCAATAGGATGCAAAGATCAATGCAAAAAATT  
GTTATATATGAACATATAACTGGAGTCGTCAAAAAGCAAATTAAGAAAGAAATTGGACGTTAG  
AAGTTGTCAATTTAAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAAATAAAAAA  
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

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## **FIGURE 206**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD  
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK  
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW  
WRHLVAGGGAGAVSRTCTAPLDRLKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI  
NVLKIAPESAIKFMAYEQIKRLVGSQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMAL  
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIIPYAGIDLAVYETLKNAWLQHYAVNS  
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG  
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Transmembrane domain:**

amino acids 284-304, 339-360, 376-394

#### **Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

#### **N-glycosylation site.**

amino acids 129-133, 169-173

#### **Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

**FIGURE 207**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT  
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG  
CAATTGCACTCATCATTGGCTTTGGTATTTTCAAGGAGACACTCCATCACAGTCACTACTGTC  
GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAA  
ACTTTCTGATATCGTGATAACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA  
AAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTTCAAGGGCCGGACAGCAGTGTTT  
GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC  
TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA  
AAACTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG  
CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCA  
GGGAGCCAACCTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA  
TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA  
AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG  
TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTGCCATCAGCT  
GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAATGTGCCTTGGCCACAAAAAAG  
CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG  
TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA  
AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAA  
GACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGAGTGATAAG  
TAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT  
GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG  
TAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCA  
CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG  
GGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTTTTATGATGCTTCCAAAGGTGCCT  
TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA  
ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA  
AA

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**FIGURE 208**

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI  
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD  
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD  
QGANFSEVSNTSFELNSENVTMKVVSVLNVTINNTYSCMIENDIAKATGDIKVTESEIKRR  
SHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

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	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
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[illegible]

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**FIGURE 210**

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQC  
GSLLYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSS  
FPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

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**FIGURE 211**

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG  
GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT  
TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT  
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGGCATCCTCG  
TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT  
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG  
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT  
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT  
GCTGAAGAACAACCTTTCATTTTGTAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG  
CGATGCCCTGGACCCTCCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG  
AATCTAATGGAACCTTCCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC  
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC  
CAACGTCAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCA  
TCTTTCGAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT  
TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG  
GGGACTGCTGCCCTGAGGTCTGGGGCTGCACCTTGCCCAGCACCCCATTTCTGCTTCTCTG  
AGGTCCAGAGCACCCCCTGCGGTGCTGACACCCTCTTTCCCTGCTCTGCCCCGTTTAACTGC  
CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA  
AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 212**

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLETPVR  
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE  
CPACYESNGTSCRGKPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK  
TLGGVIFRKFEKANVNSLTPTSAPTTSNHNVGSKASLYLLALASLLLRGLLP

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**FIGURE 213**

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA  
GGGCTTGCCTCACTGGCCACCCTCCCAACCCCAAGAGCCCAGCCCC**ATG**GTCCCCGCCGCCG  
GCGCGCTGCTGTGGGTCTCTGCTGAATCTGGGTCCCCGGGCGGGCGGGGGCCCAAGGCCTG  
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCAG  
CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA  
ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC  
ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA  
GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCCACTGCGACTCCCA  
ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG  
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC  
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCTCACCCACAG  
CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC  
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT  
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGACCTATCAACAATGTC  
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT  
GCCTCTCAGAGCACCACCAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG  
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTTTGAAACGGGTCA  
GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA  
GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT  
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTGTAGTACAGAAAAACAAACTGGAAAA  
CACAA

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**FIGURE 214**

MVPAAGALLWVLLLNLGPRAGAQLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRI  
ILEDENDAMADADRLAGPAAAELLAATVSTGFSSAINEEDGSSEEGVVINAGKDSTSREL  
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP  
SPSPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC  
TYQQPCPNRLREECPLDTSLCTDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA  
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

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**FIGURE 215**

CCCCGGTTCGACCCACGCGTCCGGGGAGAAAGGATGCGCGGCTGGCGGCGCGGTTGGTCCTGCTAGCTGGGGCA  
GCGGCGCTGGCGAGCGGCTCCAGGGCGACCGTGAGCCGGTGTACCGCGACTGCGTACTGCAGTGCAGAGAGCA  
GAACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT  
GTCGGGACGACTGTAAGTATGAGTGTATGTGGGTACCGTTGGGCTCTACCTCCAGGAAGGTCACAAAGTGCCT  
CAGTTCCATGGCAAGTGGCCCTTCTCCCGTTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCGTTTCT  
CAATGGCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCCATGTACCACA  
CCTGTGTGGCCTTCGCCTGGGTGTCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGAC  
CTCACAGAGAAAATGGACTACTTCTGTGCCTCCACTGTCATCCTACACTCAATCTACCTGTGCTGCGTCAGGAC  
CGTGGGGCTGCAGCACCCAGCTGTGGTCAGTGCCTTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCT  
CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG  
GTGTGGTGGCTGGCCTGGTGCCTGTGGAACCAGCGGCGGCTGCCTCACGTGCGCAAGTGCCTGGTGGTGGTCTT  
GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCCACCGCTCTTCTGGGTCTGGATGCCCATGCCA  
TCTGGCACATCAGCACCATCCCTGTCCACGTCCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG  
AAGGAATCAGAGGACAAGTTCAAGCTGGACTGAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCC  
GCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTCTTGAACTTGGACATGA  
AGGATGTGGGCCCAGAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG  
AAGGCCTCCCAGCATCTGGGACTCGAGAGTGGGAGCCCTCTACCTCCTGGAGCTGAACTGGGGTGGAACTGA  
GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCTGTTTCTCCTCCCAACAGCCTCCTCCCACTCCCAAGCTG  
CCTGGCTGGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGGACCACAGGCCTTAGGGATACAGGGGGTCCC  
CTTCTGTTACACCCCCACCTCCTCCAGGACACCACTAGGTGGTGTGCTGGATGCTTGTCTTTGGCCAGCCAA  
GGTTCACGGCGATTCTCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCAACCTGACC  
GTTGCCCTAGCCAGGTTCACAGAGGCCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCCAGGGCA  
AGGATCCTGTGCTGCTGTCTGGTTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGG  
TGACAGGGCCGTGAGCATGGGCCTGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTTGT  
CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTCAGGGGGTGGGTGTGTTAGCCTGGGTAGGGGAACGTGTG  
TGCGCGTGTGTTGGGCATGTGAGATGAGTGAATGTGTCCACAGTTGAGAGGTGGAGCAGGAT  
GAGGGAATCCTGTACCATCAATAATCACTTGTGGAGCGCCAGCTCTGCCAAGACGCCACCTGGGCGGACAGC  
CAGGAGCTCTCCATGGCCAGGCTGCCTGTGTGCATGTTCCCTGTCTGGTGCCCTTTGCCCGCCTCCTGCAAAAC  
CTCACAGGGTCCCCACACAACAGTGCCTCCAGAAGCAGCCCTCGGAGGCAGAGGAAGGAAAATGGGGATGGC  
TGGGGCTCTCTCCATCCTCCTTTCTCCTTGCCCTTCGCATGGCTGGCCTTCCCTCCAAAACCTCCATTCCCT  
GCTGCCAGCCCTTTGCCATAGCCTGATTTTGGGGAGGAGGAAGGGGCGATTTGAGGGAGAAGGGGAGAAAGCT  
TATGGCTGGGTCTGTTTCTTCCCTTCCAGAGGTCTTACTGTTCCAGGTGGCCCCAGGGCAGGCGGGCC  
ACACTATGCCTGTGCCCTGGTAAAGGTGACCCCTGCCATTTACCAGCAGCCCTGGCATGTTCTGCCCCACAGG  
AATAGAATGGAGGGAGCTCCAGAACTTTCATCCCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTTG  
CTCTGCCCTGACCCCTTGTCCCTCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGGAAGTGGGTG  
GCCTGCGCTAGCTTCTTTTGATACTGAAAACCTTTTAAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAA  
TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

## **FIGURE 216**

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW  
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR  
YRTFVPASSPMYHTCVAFWVSLNAWFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR  
TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR  
RLPHVRKCVVVVLLLQGLSLELLDFPPLFWVLDAHAIWHISTIPVHVLFFSFLEDDSLYLL  
KESEDKFKLD

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

#### **N-glycosylation site.**

amino acids 40-44

#### **N-myristoylation site.**

amino acids 43-49

#### **CUB domain proteins profile.**

amino acids 285-302

#### **Amiloride-sensitive sodium channels proteins.**

amino acids 162-186

[illegible]

**FIGURE 218**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEHEEL  
DAEVLEV FHP THEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN  
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV  
RLINKFNSSSSSLEEKIAALFDLEYVHQM DNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF  
VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL  
GGLQVLR TLVQEKGTEVLAVRVVTL LYDLVTEKMF AEEEEAE LTQEMSPEKLQQYRQVHLLPG  
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS  
LELQDGEDEGYFQELLGSVNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340

**FIGURE 219**

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCC  
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTCGCGTTGCCACCCCA  
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCTGTCCTGGTCAGGCCCCCACCCTCC  
 TTCCACCTGACCAGCC**ATG**GGGGCTGCGGTGTTTTTTCGGCTGCACTTTCGTCGCGTTTCGGC  
 CCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGT  
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGG  
 TCCATGTGACCGACCGGTGAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTTGGTGCTGCT  
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA  
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT  
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT  
 GATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCTGACTTC  
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG  
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCTGGTGGTTGGGAGTCACCTACTGACATCG  
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT  
 TTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCC  
 TCTTGTGTAAGGACT**TGA**CTACCTGGACTGATCGCCTGACAGATCCCACCTGCCTGTCCACTG  
 CCCATGACTGAGCCCAGCCCCAGCCGGGTCCATTGCCACATTCTCTGTCTCCTTCTCGTC  
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTTGTGACCGTTAGTCTCTAAGCTT  
 TACCAGGAGCAGCCTGGGTTTACGCCAGTCAGTGACTGGTGGGTTTTGAATCTGCACTTATCCC  
 CACCACCTGGGGACCCCTTGTGTTGTGTCCAGGACTCCCCCTGTGTGAGTGCTCTGCTCTCAC  
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGTCAGGCCGACGGCAGGAGGACAGTCGGGTGAT  
 GGTGTATTCTGCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC  
 CTGGGGTGCCCTCCTGATGTCCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAG  
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA  
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTTCTC  
 AGGCTGAGGGGGGAACCATTTTTTGGTGTGATAAATACCCTAAACTGCCTTTTTTTCTTTTTT  
 GAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTTCTAACCCTCCTTGGGCTATATTTTCTC  
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTTCGGTCCCTTTCTCCTTGGTCCCAGACCTT  
 GGGGGAAAGGAAGGAAGTGCATGTTTGGGAACTGGCATTACTGGAACATAATGGTTTTAACCT  
 CCTTAACCACCAGCATCCCTCCTCTCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGC  
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGG  
 GAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGT  
 ATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATCAAGGTGATTGTGATTTTGACT  
 AATAAAAAAGAATTTGTAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 220**

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR  
SDARLQYGLLIFGAAVSVLLQEVRFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLS  
FGIISGVFSVINILADALGPGVVGIIHGDSPPYFLTSAFLTAAIILLHTFWGVVFFDACERRR  
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLCKD

090444-444444



AAGCTGGTTTAAAGGAAGCAGAGGAGGGTTAGATTTCGTTGAGTGAGGACGGAAGATCAACCCA  
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGNATCATCAGTGGTGTNT  
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC  
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

GACCGACCGTTTCAGATGCCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG  
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG  
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN  
TGGTNTTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTTGGNTGATGCAN  
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAATTCTGAATTCAGCCTTT  
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA  
GAGGAG

**FIGURE 223**

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTCCCTTTCCCCG  
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCCACGCGGACTCC  
CCAGNTGGNGCGCCCTTCCCATTTCCTGTCCTGGTCAGGCCCCCACCCCCCTTCCCACNTG  
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTCGGCCCCGGCCTTCG  
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA  
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC  
CGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTTGGTGCTGCTGTCTCTGTCC  
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA  
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG  
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTTG  
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

**FIGURE 224**

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTTCCCNTTCCCCGGGG  
TCTGGGGGTGACATTGCACCGCGCCCNTCGTGGGGTCGCGTTGCCACCCCACGCGGACTCCC  
CAGNTGGCGCGCCCCTCCCATTTGCCTGTCCTGGTCAGGCCCCCACCCTTCCCACCTGA  
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTTCGGGCCCCGGCCTTC  
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGC  
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA  
CCGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC  
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT  
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG  
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT  
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

**FIGURE 225**

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAG  
TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCCACC  
TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG  
TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCTCCTTGCCCTGTCTGGAGGCTGCT  
AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT  
CCTTGTGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC  
CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTCACAGAGCATGTT  
CTCGCCAACAATGATGTTTCCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA  
GGACCTGGGAGCTGGGGCCGGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA  
ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC  
CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAG  
GAAGAAAGTTTTAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGC  
AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCTGGCTACTCCCACCCTGGCCACTCT  
AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTCGTCCCCTAAAGATGTCAGACCCAT  
CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA  
CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGT  
CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA  
CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC  
TGCAGGGACTCGTGTCTGGGGAGATTACCCTTGTGCCCCGGCCCAACAGACCGGGTGTCTAC  
ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC**TGA**GTCAT  
CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG  
ACCCTCATTCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCT  
CCTGGACTCAGGGTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGG  
GAACAATTTCCAAAACCTGTCCAGGGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCAT  
CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA  
CTGAGAAGTGGAATAAAAAA

**FIGURE 226**

MATARPPWMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD  
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS  
PVYESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRIRPTKDVRPINVSSHCP SAGTKCL  
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGR DSCQGD SGGP  
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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**FIGURE 227**

**ATG**GTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCCAACTTGAGGACCGGCCGCGGA  
 CAAGCCGCAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGGCCCTGGCTGTGC  
 TGCTGGCTGTAGCTGTACCGGTGCCGTGCTCTTCTGAACCACGCCCACGCGCCGGGCACG  
 GCGCCCCACCTGTCGTACGACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTCACTGTGGA  
 AAGGGCGGACAGCTCGCACCTCAGCATCCTCATTGACCCGCGCTGCCCCGACCTCACCAGACA  
 GCTTCGCACGCCTGGAGAGCGCCAGGCCTCGGTGCTGCAGGGCGCTGACAGAGCACCAGGCC  
 CAGCCACGGCTGGTGGGCGACCAGGAGCAGGAGCTGCTGGACACGCTGGCCGACCAGCTGCC  
 CCGGCTGCTGGCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG  
 GCACGCTGGGCCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGCCGCCTCATCCAGCTTCTC  
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTACAGCGACATCCTGGATGCCCT  
 GCAGAGGGACCGGGGGCTGGGCCGGCCCCGCAACAAGGCCGACCTTCAGAGAGCGCCTGCCC  
 GGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCCGGCCCCGAGACTGTCTGGACGTCTCT  
 CTAAGCGGACAGCAGGACGATGGCGTCTACTGTCTTTCCACCCACTACCCGGCCGGCTT  
 CCAGGTGTACTGTGACATGCGCACGGACGGCGGCGGCTGGACGGTGTTCAGCGCCGGGAGG  
 ACGGCTCCGTGAACCTTCTTCCGGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTCACC  
 GGGGAGCAGCTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGAGCT  
 GCACGTGGACTGGAGGACTTTGAGAATGGCAGGGCCTATGCCGCTACGGGAGCTTCGGCG  
 TGGGCTTGTCTCCGTGGACCTGAGGAAGACGGGTACCCGCTCACCCTGGCTGACTATTCC  
 GGCACGTGCAGGCGACTCCCTCCTGAAGCACAGCGGCATGAGGTTTACCACCAAGGACCGTGA  
 CAGCGACCATTCAGAGAACAACCTGTGCCGCTTCTACCGCGGTGCCTGGTGGTACCGCAACT  
 GCCACACGTCCAACCTCAATGGGCAGTACCTGCGCGGTGCGCACGCTCCTATGCCGACGGC  
 GTGGAGTGGTCCCTCCTGGACCGGTGGCAGTACTCAAGTTCTCTGAGATGAAGATCCG  
 GCCGGTCCGGGAGGACCGCT**TAG**ACTGGTGCACCTTGTCTCTTGGCCCTGCTGGTCCCTGTGCG  
 CCCATCCCCGACCCACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCCTGGCGGAC  
 CCACTCTCCAGTAGGGAGGGGCCGGGCCATCCCTGACACGAAGCTCCCTGGGCCGGTGAAGT  
 CACACATCGCCTTCTCGCCGTCCCCACCCCTCCATTTGGCAGCTCACTGATCTCTTGCCTC  
 TGCTGATGGGGCTGGCAAACCTTGACGACCCCAACTCCTGCCTGCCCCACTGTGACTCCGG  
 TGCTGTTTGGCGTCCCCTGGCCAGGATGGTGGAGTCTGCCCCAGGCACCTCTGCCCTGCC  
 GGCCAAATACCCGGCATTATGGGGACAGAGAGCAGGGGGCAGACAGCACCCCTGGAGTCCTC  
 CTAGCAGATCGTGGGGAATGTGAGGTCTCTCTGAGGTGAGGTCTGAGGCCAGTATCCTCCAG  
 CCTCCCAATGCCAACCCCAACCCGTTTCCCTGGTGCCCAGAGAACCCACCTCTCCCCCAA  
 GGGCCTCAGCCTGGCTGTGGGCTGGGTGGCCCCATCCTACCAGGCCCTGAGGTGAGGATGGG  
 GAGCTGCTGCCTTTGGGGACCCACGCTCCAAGGCTGAGACCAGTTCCCTGGAGGCCACCCAC  
 CCTGTGCCCCGGCAGGCCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCACCTGCTCTCTG  
 TCTCAAATGAGGCCCAACCCATCCCCACCCAGCTCCCGGCCGTCTCTACCTGGGGCAGC  
 CGGGGCTGCCATCCCATTTCTCCTGCCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT  
 GGACTGCGCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGGCCTAGGCAGGGCTGGGATGAG  
 GCTTGTACAACCCCCACCACTTCCAGGGGACTCCAGGGTCTGAGGCCCTCCAGGAGG  
 GCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCCATGAGGAGGCCAACCCCTGCC  
 ATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGGCCGAGTGGTCAAGGGACAGGGA  
 CCACCTCACCGGGCAAATGGGGTCCGGGGGACTGGGGCACCAGACCAGGCACCACCTGGACA  
 CTTTCTTGTGAATCCTCCCAACACCCAGCAGCTGTCTATCCCCACTCCTTGTGTGCACACA  
 TGCAGAGGTGAGACCCGCAGGCTCCCAGGACCAGCAGCCACAAGGGCAGGGCTGGAGCCGGG  
 TCCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGCGTGCGTTACGTGAGGCCAGATGCAGGG  
 CGGCTTTTCCAAGGCCTCCTGATGGGGGCTCCGAAAGGGCTGGAGTCAGCCTTGGGGAGCT  
 GCCTAGCAGCCTCTCCTCGGGCAGGAGGGGAGGTGGCTTCTTCCAAAGGACACCCGATGGCA  
 GGTGCCTAGGGGTGTGGGGTTCGGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAAA  
 AACAAATAAATTTGACTTGGCACCACTGGGGGTTGGTGGGAGAGGCCGTGTGACCTGGCTCTC  
 TGTCCAGTGCCACCAGGTCATCCACATGCGCAG

**FIGURE 228**

MVNDRWKTMGGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT  
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA  
QPRLVGDOEQELLDTLADQLPRLRARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL  
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL  
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT  
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS  
GTAGDSSLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG  
VEWSSWTGWQYSLKFSEM KIRPVREDR

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GCAGT CAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT  
TGCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCT  
CACCGCTGTAGGAATCCAG**ATG**CAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG  
ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC  
CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC  
TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACC  
AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC  
CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC  
TGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG  
AACAAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG  
GACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAACAAGAAGA  
CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT  
TGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACCTCTGAACTG  
TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG  
GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA  
TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC**TGA**ATTCGCC  
CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT  
TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG  
TTTCCTGTT CAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA  
AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCATAATGTCATCTGCCTTCTTG  
GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT  
GTCTTCCTTACACTTGGTGGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC  
ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTCCCAGATTGTACC  
AGCAAATACACAAGGAATTCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT  
CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG  
AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCCTGTGTCCATTAAAGACTCTGATAATTG  
TCTCCCCTCCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG  
AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCA  
TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAG  
GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

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**FIGURE 230**

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLL  
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE  
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS  
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD  
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

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**FIGURE 231**

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG  
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG  
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG  
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTA  
CTACCAGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATA  
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT  
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA  
AGTNTCCTCATNTACTATACACACACCACTTCCC

CGCCGAGCGCAAGAACCCTGCGCAGCCCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC  
CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGCGGGG  
CCCCGAGCCCTCCGGATCCGCCCCCTCCCCGGTCCCGCCCCCTCGGAGACTCCTCTGGCTGCT  
CTGGGGGTTTCGCCGGGGCCGGGGACCCGCGGTCCGGGCGCC**ATG**CGGGGCATCGCTGCTGCTG  
TCGGTGCTGCGGCCCGCAGGGCCCGTGCCCGTGCGCATCTCCCTGGGCTTCACCCTGAGCCT  
GCTCAGCGTACCTGGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCCAACCTGGAGACTCTG  
AGCTGCCGCCGCGCGGCAACACCAACGCGGCGCGCCGGCCCAACTCGGTGCAGCCCGGAGCG  
GAGCGCGAGAAGCCCCGGGGCCGGCGAAGGCGCCGGGGAGAATTGGGAGCCGCGCGTCTTGCC  
CTACCACCCTGCACAGCCCGGCCAGGCCGCAAAAAGGCCGTGAGGACCCGCTACATCAGCA  
CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC  
ACGCTGGGCGTGCCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTTCCTGAC  
GGGCGCACGGGGCCGCCGGGGCCCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC  
CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC  
TGGTTCTTCTGGTGCTGACACCACCTACACCGAGGCGCACGGCCTGGCACGCCTAACTGG  
CCACCTCAGCCTGGCCTCCGCCGCCACCTGTACCTGGGCGGGCCCCAGGACTTCATCGGCG  
GAGAGCCCCACCCCGGCCGCTACTGCCACGGAGGCTTTGGGGTGCTGCTGTGCGCATGCTG  
CTGCAACAACTGCGCCCCCACCTGGAAGGCTGCCGCAACGACATCGTCAGTGCGCGCCCTGA  
CGAGTGGCTGGGTGCTGCTGCTGCTGATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGG  
GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGCAAGAGGGGACCCTCAT  
TTCCGAAGTGCCCTGACAGCCACCCTGTGCGTGACCTGTGCACATGTACCAGCTGCACAA  
AGCTTTCGCCCGAGCTGAACTGGAACGCGACGTACCAGGAGATCCAGGAGTTACAGTGGGAGA  
TCCAGAATACCAGCCATCTGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATT  
CCAGCACCATCCCGCCCGGCCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA  
GCACGCTTTCTCCTGCGCCGATGGCTCACCCCGCTGCCCACTGCGTGGGGCTGACCGGGCTG  
ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCCGGCCTTG  
CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGA  
ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCCAGGGAGGCCCGCCGCCCTCACTC  
GCCGAGTGCACTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCCCTGTGCCCTATGTCACT  
GAGGCCTCACGTCTCACTGTGCTGCTGCTAGCTGCGGCTGAGCGTGACCTGGCCCTTG  
CTTCTTGGAGGCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC  
TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATGCAGATGTCTTCGCACCT  
GTCAAGGCCACAGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGGTGCCATGGCTCAG  
TGTGCAGACAGCCGCACCCTCACCACTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCGC  
TGGACACACTGTTCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCTGAACCGC  
TGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCCAAGCCTTCCA  
CCCAGGTGTGGCCCCACCACAAGGCCCTGGGCCCCCAGAGCTGGGCGGTGACACTGGCCGCT  
TTGATCGCGCAGGCAGCCAGGCCTGCTTCTACAACCTCCGACTACGTGGCAGCCCGTGGG  
CGCTTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT  
GTTCTTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT  
ACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGTACCACCGCTGCCTCCAGAGC  
GTGCTTGAGGGCCTCGGCTCCCGAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG  
CAACAGCACCT**TGA**CCCCACCCTGTCCCCGTGGGCCGTGGCATGGCCACACCCACCCCACTT  
CTCCCCCAAACACAGAGCCACCTGCCAGCCTCGCTGGGCAGGGCTGGCCGTAGCCAGACCCC  
AAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTGGGTCCCTGGGCTCTGGACAAGCACTGGG  
GGACGTGCCCCCAGAGCCACCCACTTCTCATCCCAAACCCAGTTTCCCTGCCCCCTGACGCT  
GCTGATTGCGGCTGTGGCTCCACGTATTTATGCAGTACAGTCTGCCTGACGCCAGCCCTGC  
CTCTGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTTGGGAAGGAGGAGCTGAGGAGGGG  
GCATCTCCCAACTTCTCCCTTTTGGACCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA  
AGTGTGGAAAAA

**FIGURE 233**

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP  
NSVQPGAEREKPGGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRLLVAVL  
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL  
QHGDDEFDWFLLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG  
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHYSHLELSPGEP  
VQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAELETTYQEIQELQWEIQNTSHLAVDGDRA  
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLTAL EELN  
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI  
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA  
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTL FLLAGPDTVL  
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGPGPPELGRDTGRFDRQAASEACFYNS  
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLVLR AVEPALLQRYRAQTCSARLSEDL  
YHRCLQSVLEGLGSRTQLAMLLFEQEQGNST

**FIGURE 234**

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT  
TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT  
AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTTAGAAAGCTTGATTTCCCTTTGAAGATGAAAG  
ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA  
CTGTATCCACCCAAATGTCACCGATTTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA  
GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG  
AGGGTTGCTCAACGCCCCGCCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG  
GCGGAGGCGGGGCGATGATTGTGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT  
TTCCCCGCCCCTGAGACCCTGCAGCACCATCTGT**ATG**GCGGCTGGGCTGTTTGGTTTGAGC  
GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCCGCGTCCGCTGGGA  
ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGGCCCCCAGAAC  
CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCCA  
GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCGACTTGTCTTCTT  
CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA  
GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC  
CTTCCCATCATGGAATCCAACCTGCTTCGACCCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**  
**A**CCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCCTGCCTGCCATTCTGAC  
CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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**FIGURE 235**

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE  
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER  
LVKYREANGLPIMESNCFDPSKIQLPED

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**FIGURE 236**

GGCGGCTGGGCTGTTTGGTTTGGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC  
TCCCGGCCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT  
GTGGCGGGAAAGCGGCCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA  
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTTGGACG  
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC  
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT  
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAC TGCTTCGACCCCAGCA  
AGATCCAG

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**FIGURE 237**

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCCTGTTGCTCCTGGGGCCCCGGCGGCTGGTGCCT  
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTTGTTCATCACCCCGCTGCCTTCCGGGG  
 ACGTAGCCGCCACATTCCAGTTCCGCACGCGCTGGGATTTCGGAGCTTCAGCGGGAAGGAGTG  
 TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA  
 GCTGCACCTGTCAATTCACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCTTCCTGC  
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA  
 TCTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA  
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG  
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC  
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTCTCTGTGCTGCTGAAGGCAGA  
 TCGCTTGTTCCACACCAGCTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG  
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCAGTTGTATTTGATGCCTTC  
 ATCACGGGGCAGGGAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA  
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACAACCAGGACA  
 ACGAGACATTAGAGGTGCACCCACCCCCGACCACTACATATCAGGACGTCATCCTAGGCACT  
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT  
 CAACATCCAGCTCAAGTGGAAGAGACCCCCAGAGAATGAGGCCCCCCCAGTGCCCTTCCTGC  
 ATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC  
 AACACCCACCCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG  
 GCTGTATGTGCACACCCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC  
 ACTACCAGCCTGCCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTTCAGCTGCCG  
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA  
 CACGCCAGATCCTAACCATGGCTTCTATGTCAGCCCATCTGTCCTCAGCGCCCTTGTGCCCA  
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCCCTCTTCAACAGCCTGTTCCCA  
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC  
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT  
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT  
 GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACTCT**GA**ATT  
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT  
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTCAGGGC  
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGTAATTTGAATTAA  
 CTTAGAAATTCAATTCCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA  
 AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACACAGAAAGGTC  
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGGA  
 TGGAGTTTACTGTTTGTGGAATAAAAAACGGCTGTTTCCGTGGAAAAAAAAAAAAA

**FIGURE 238**

MPLALLVLLLLGPGGWCLAEP PRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY  
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDKSWK  
ELSNVLSGIFCASLNFIDSTNTVTPTASF KPLGLANDTDHYFLRYAVLPREVVCTENLTPWK  
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSSISWELRQTL SVVFDAFITG  
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT  
YAIYDLLDTAMINNSRNLNIQLKWKRPPE NEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH  
PYRAFPVLLLLDTVPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDR LQPHLLEMLIQLPANS  
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAKPVDWEESPLFNSLFPVSD  
GSNYFVRLYTEPLL VNLPTPDFSMPYNVICLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLA  
KRLANLIRRARGVPPL

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**FIGURE 239**

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG  
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCCAGCTGACAACGTACGC  
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG  
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA  
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC  
TCCTCCTCTACCAGGTGTCCTCAGAAATGAATGCTGGGTCTTTCTACCTCTGGGGGTCACTC  
TCACTTGGCACCTGCCCCCTGAGGGTCTTGAGACTTGGAATATGGAAGAAGCAATACCCAACC  
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAG  
TCCAGACCCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT  
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC  
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCCTCACCAGATG  
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCCAGCCTCTAGAAGTGTAAAGAAATAAATAT  
TTGCTGTTTATAATCCAA

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## **FIGURE 240**

MGSSSFVLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC  
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

**Signal sequence:**

amino acids 1-19

**N-myristoylation sites:**

amino acids 23-29, 27-33, 32-38, 102-108

**WAP-type 'four-disulfide core' domain signature:**

amino acids 49-63

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AAACCTCAGCACTTGC CGGAGTGGCTCATTTGTTAAGACAAAGGGTGTGCACCTTCTTGGCCAGG  
AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC  
TCTAGAACCCGACCCACCACC**ATG**AGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGG  
CGTCCAGTGGTCCTTGCTTCTGGCTGTCTTGCTTCTTCTTCTTCTCGCCTTGCCCTCTTTTA  
TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAGAAAGGTCT  
CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA  
TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCCAAGGCCACACCA  
CCGGAGACAGAGGAAAGGAGGCCAACCCAGGCACCGCCGAGGAGCAGGACAAGGTGCCCCAC  
ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC  
ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC  
AGGACACAAAGACGACCCAAAGGAAATGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG  
GTGTCTAGAGAAGCACCAGGGCAAAGCGCAACCCACAGCCAAGACGCTCATTTCCCAAAGTCA  
GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACGAGAAAGGAGTGACCA  
CAGCAGTCATCCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTTGGCCCTTTCCAG  
AGCCCCACGACGCAGAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG  
GGATTTTGAGGAAAAATACAGCTTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTG  
TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAAACTCTTTCTGCCCAACCTCACTCTC  
TTCTTGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACC  
CTTTGGCTTCATGGAGCTCAACTACTCCTTGCTGCAGAAGGTCGTGACACGCTTCCCTCCAG  
TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGT  
GCCGTGGTGGGCAACGGGGGCATCCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCA  
GCACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGGACTC  
GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT  
CGGGGTTTCAAGAACGTGCCTCTTGGAAGGACGTCCGCTACTTGCACTTCTTGGGAAGGCAC  
CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT  
TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG  
TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGA  
TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC  
AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT  
CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA  
GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCCTGGTC  
CCGGAAC TGCCAAAGCCAAGAACTGAACCGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC  
CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA  
GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT  
GGCAAATGGCTAATTGAGGTTCTGAAGTTCTTCAGTACATTGCTGTAGGTCTGAGGCCAGG  
GATTTTTTAATTAATGGGGTGATGGGTGGCCAATACCACAATTCTGCTGAAAAACACTCTT  
CCAGTCCAAAAGCTTCTTGATACAGAAAAAAGAGCCTGGATTTACAGAAACATATAGATCTG  
GTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC  
AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGGTCTATACTTGTCTTG  
TCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT  
GTCCATGGAAAGGCCAAATAAATTTTCTACAGTGAAAAA

**FIGURE 242**

MRSCLWRCRHL SQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHRQRTENIKERSLQSLAKP  
KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW  
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQG  
KAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPKKKPQATPPPAPFQSPPTQORN  
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLEFLDSRHF  
NQSEWDRLEHFAPPFQGMELNYSLVQKVVTFRFPVPQQQLLLASLPAGSLRCITCAVVGNGG  
ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGF TAFSLTQSLILGNRGFKNVP  
LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLHPDFL  
RYMKNRFLRSKTL DGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW  
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRP GPGTAKAKN

**Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Lumenal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

**FIGURE 243**

CGATGCGCGGACCCGGGCACCCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG  
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT  
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA  
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT  
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC  
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG  
ACAAGAGATTTATTTTTGCAGACAGACTCTTCCATAAGTCCTTTGAGTTTTGTATGTTGTTG  
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

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**FIGURE 244**

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT  
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

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GGGCTGGGCCCCCGCCGACGCTCCAGCTGGCCGGCTTGGTCTTGCGGTCCCTTCTCTGGGAGG  
CCCGACCCCGGCCGCGCCAGCCCCACCA**ATG**CCACCCGCGGGGCTCCGCCGGGGCCGCGCCG  
CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCCTGGTGCTGGCCGGCGAGGACTGCCT  
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTACCTTCT  
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG  
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT  
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT  
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC  
CCAGTGACAGCCAGTATACCCATAACCCCAAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC  
TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC  
CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC  
**TGA**AGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT  
CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA  
GCCAAGCCCTGGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA  
ACTATGAGGGGTGGGGGGAGGGCTTGGAATTATGGGCTATTTTTTACTGGGGGCAAGGGAGG  
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCAG  
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT  
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCACTGGCCACATCTCTGGCCTG  
CTAGATTAAAGCTGTAAAGACAAAA

**FIGURE 246**

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFC CGTCYHRYC  
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCF LCSCCYLYRRRQQLQSP  
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP  
YMPPQPSYPGA

**Transmembrane Domains:**

amino acids 10-28, 85-110

**N-glycosylation Site:**

amino acids 38-41

**N-myristoylation Sites:**

amino acids 5-10, 88-93

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GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGGCGCAAGGGTGAGGGGCGGCCCCAGAA  
 CCCCAGGTAGGTAGAGCAAGAAG**ATG**GTGTTTCTGCCCTCAAATGGTCCCTTGAACCATG  
 TCATTTCTACTTTTCTCACTGTTGGCTCTCTTAACCTGTGTCCACTCCTTCATGGTGTGAGAG  
 CACTGAAGCATCTCCAAAACGTAGTGTATGGGACACCATTTCCTTGGAAATAAAATACGACTTC  
 CTGAGTAGCTCATCCCAAGTTCATTATGATCTCTTGATCCATGCAAAACCTTACCACGCTGACC  
 TTCTGGGGAAACCAGAAAGTAGAAATCACAGCCAGTCAGCCCCAACAGCACCATCATCTGTCA  
 TAGTCACCACCTGCAGATATCTAGGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGGCTATCGG  
 AAGAACCCCTGCAGGTCTGGAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCGAG  
 CCCCTCCTTGTGGGGCTCCCGTACACAGTTGTCTATTCACTATGCTGGCAATCTTTCGGAGAC  
 TTTCCACGGATTTTACAAAAGCACCTACAGAAACCAAGGAAGGGAACTGAGGATACTAGCAT  
 CAACACAATTTGAACCCCACTGCAGCTAGAATTGGCCTTTCCCTGCTTTGATGAACCTGCCTTC  
 AAAGCAAGTTTCTCAATCAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCCAATATGCC  
 ATTGGTGAAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGA  
 AGATGAGCACCTATCTGGTGGCCTTCATCATTTTCAGATTTTGAGTCTGTGAGCAAGATAACC  
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCCAGACAAGATAAAATCAAGCAGATTATGC  
 ACTGGATGCTGCGGTGACTCTTCTAGAATTTATGAGGATTATTTCAGCATACCGTATCCCC  
 TACCCAAACAAGATCTTGCTGCTATTCCCGACTTTCAGTCTGGTGCTATGGAAAACCTGGGGA  
 CTGACAACATATAGAGAATCTGCTCTGTTGTTTGATGCAGAAAAGTCTTCTGCATCAAGTAA  
 GCTTGGCATCAGAGTACTGTGGCCCATGAACCTGGCCCACCAGTGGTTTGGGAACCTGGTCA  
 CTATGGAATGGTGAATGATCTTTGGCTAAATGAAGGATTTTGCCAAATTTATGGAGTTTGTG  
 TCTGTCAGTGTGACCCATCCTGAACGAAAGTTGGAGATTATTTCTTTGGCAAATGTTTGA  
 CGCAATGGAGGTAGATGCTTTAAATTCTTCACACCCTGTGTCTACACCTGTGGAAAATCCTG  
 CTCAGATCCGGGAGATGTTTGATGATGTTTCTTATGATAAGGGAGCTTGTATTCTGAATATG  
 CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAAGCA  
 TAGCTGATAAAAATCAAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAG  
 ATGGTGTA AAAAGGGATGGATGGCTTTTGCTCTAGAAGTCAACATTCATCTTCACCTCACAT  
 TGGCATCAGGAAGGGGTGGATGTGAAAACCATGATGAACACTTGACACTGCAGAGGGGTTT  
 TCCCCTAATAACCATCACAGTGAGGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA  
 AGGGCTCTGACGGCGCCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTCATCACC  
 AGCAAATCCAACATGGTCCATCGATTTTGTCTAAAAACAAAACAGACATGTGCTCATCTCTCC  
 AGAAGAGGTGGAATGGATCAAATTTAATGTGGGCATGAATGGCTATTACATTGTGCAATTACG  
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAAGGAACACACACAGCAGTCAGCAGT  
 AATGATCGGGCAAGTCTCATTAAACAATGCATTTTCAGCTCGTCAGCATTGGGAAGCTGTCCAT  
 TGAAAAGGCCCTTGGAATTTATCCCTGTACTTGAAACATGAAACTGAAATTATGCCCGTGTTC  
 AAGGTTTGAATGAGCTGATTTCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGT  
 GAAACTCAATTC AAGGCCCTTCCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG  
 GACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCGGAGTGAACCTACTACTCCTCGCCTGTG  
 TGCACAACCTATCAGCCGTGCGTACAGAGGGCAGAAGGCTATTTCAGAAAGTGGAAGGAATCC  
 AATGGAAACTTGAGCCTGCCGTGTCGACGTGACCTTGGCAGTGTTTGCTGTGGGGGCCCCAGAG  
 CACAGAAGGCTGGGATTTTCTTTATAGTAAATACAGTTTCTTTGTCCAGTACTGAGAAAA  
 GCCAAATTTGAATTTGGCCTCTGCAGAAACCCAAAATAAGGAAAAGCTTCAATGGCTACTAGAT  
 GAAAGCTTTAAGGGGAGATAAAAATAAAAACTCAGGAGTTTCCACAAATTTCTTACACTCATTTGG  
 CAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAGGAAAAACTGGAACAAACTTG  
 TACAAAAGTTTGAACCTTGGCTCATCTTCCATAGCCACATGGTAAATGGGTACAACAAATCAA  
 TTCTCCACAAGAACCGGCTTGAAGAGGTAAGGATTTCTTCAGCTCTTTGAAAGAAAATGG  
 TTCTCAGCTCCGTTGTGTCCAACAGACAATTTGAAACCATTGAAGAAAACATCGTTGGATGG  
 ATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAAAGCTTGAACGTATG**TAA**AAA  
 TTCTTCCCTTGCCCGGTTCTGTATCTCTAATCACCAACATTTTGTGTGAGTGTATTTTCAA  
 ACTAGAGATGGCTGTTTTGGCTCCAACCTGGAGATACTTTTTTCCCTTCAACTCATTTTTTTGA  
 CTATCCCTGTGAAAAGATAAGCTGTGTAGTTTTCATGAATGGGCTTTTTCATGAATGGGCTA  
 TCGCTACCATGTGTTTTGTTCATCACAGTGTGTGCCCTGCAACGTAAACCCCAAGTGTGGGT  
 TCCCTGCCACAGAAAGATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 248**

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTFPFWNKIRLPEYVIPVH  
YDLLIHANLTTLTFTWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLE  
HPPQEQIALLAPEPLLVLGPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA  
ARMAFPCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA  
FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA  
IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL  
WLNEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD  
DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDG  
FCSRSQHSSSSSHWHQEGVDVKTMMNTWTQLRGFPLITITVRGRNVHMKQEHYMKGSDGAPD  
TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL  
TGLLKGHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP  
MYKLMEKRD MN EVETQFKAFLIRLLRDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV  
QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALC  
RTQNKEKLQWLLDESFKGDKIKTQEFQILTILGRNPVGYPLAWQFLRKNWNKLVQKFELGS  
SSIAHMVMGTTNQFSTRTRLEEVKGFFSSSLKENGSQLRCVQQTIEETIEENIGWMDKNFDKIR  
VWLQSEKLERM

**Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360

**FIGURE 249**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC  
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC  
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG  
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT  
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA  
ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAAC  
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG  
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGG  
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTC  
CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
GGCGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAT  
GAGCATTACAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCG  
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
GTGGGGAGTGGTTTGCCCTTCCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA  
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC  
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCA  
ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

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**FIGURE 250**

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI  
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRGRGGIFSNLRVQGCMPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSENTEMCEVGQVCQETL  
LLIDVGLTSTLVGKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVC  
PSC

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**FIGURE 251**

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT  
CAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG  
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG  
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCG  
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCGTCAT  
GGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC  
TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG  
AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCC  
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA  
CGCCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCA  
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCCGTGTCTTCATCGGCATCAAC  
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA  
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT  
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG  
GAGAACATGTGAGCCTCAGGCTGGGGCTGCCCATTTGGGGGCCCCACATGTCCCTGCAGGGTT  
GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG  
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG  
AAAGTGTTCTTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA  
ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC  
TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 252**

M R G N L A L V G V L I S L A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G  
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G P P G P N G E P G L P C E C S Q L R K A I G E  
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N  
G L M A A Y L A Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S  
G G W N D V A C H T T M Y F M C E F D K E N M

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**FIGURE 253**

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG  
CACCAGTGTGTGAGGGGAGCAGGCAGCGGCCTAGCCAGTTCCTTGATCCTGCCAGACCACC  
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT  
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG  
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC  
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA  
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA  
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCCTCGGCCC  
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC  
TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT  
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC  
TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGT  
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA  
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT  
CCTACATTAAAAATATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTTGCATATGAA  
AA

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## **FIGURE 254**

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK  
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK  
SSLGTEEQRPL

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 36-45

**N-myristoylation site.**

amino acids 33-39, 59-65

**Amidation site.**

amino acids 90-94

**Leucine zipper pattern.**

amino acids 43-65

**Tachykinin family signature.**

amino acids 86-92

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GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCGCTGTGCGCTGTGTGCC  
CGCGCTGTTCGCCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG  
GAGCCCTGCGGAGAGCTCAAGCGCCCAGCTCTGCCCCAGGAGCCCAGGCTGCCCCGTGAGTC  
CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCTGGGTGGTGTTCATCCCCTTGGGGC  
TGCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCTCTTAGAGGAG  
CTGCTCAGCAAATACCAGCACAAAGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA  
GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT  
CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCCGGGGGTGGGGC  
CTGGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGG  
CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTTGTT  
TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG  
AAACCTTAGACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG  
GCATGCACCATGGTGCCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT  
TGCCCAGGCTGGTCTTGAACTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG  
CTAGGATTATAGGCATGAGTCACCCGTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA  
ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC  
TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGGCCCAGGG  
CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC  
CTTAGCCCGTGTGAGCCTCACTTTCCACTTGAGAGTCTTTCCTCGCGTGGTTGCCATGACT  
GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG  
CTTTGCTAACC GGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCTCCCGGGT  
GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG  
TGGAACCTTCCTTCCTGGCTGGTTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG  
GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCAGCTATGAATGGCTT  
TTTAAACAAACCCACGTCCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC  
CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAG  
GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC  
AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAAA

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## **FIGURE 256**

MSCVLGGV IPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILML  
HNKLRGQVQPQASNMEYMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR  
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 27-31, 41-45

**N-myristoylation site.**

amino acids 126-132, 140-146

**Amidation site.**

amino acids 85-89

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**FIGURE 257**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG  
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG  
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC  
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC  
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TGA**CAGCCATTGAAGCCTG  
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT  
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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**FIGURE 258**

MSGGLPLVLLLTLGSSHGTGPGMTLQKLKESFLTNSSESSFLELLEKLCLLLHLPST  
VTLHHARSQHHVVCNT

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**FIGURE 259**

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT  
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGT  
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC  
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTTGAAAATGAATGCTTAGTGGATCTG  
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCCCTCCC  
CTCCGATTGTTCTAAATTAATTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG  
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCCTTGAAAGCCAATGGAAATACTTTTTTT  
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA  
GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT  
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT  
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC  
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA  
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGA  
ATAAAAGTTCATATCTACCC

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## **FIGURE 260**

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP  
SDCSK

**Important features:**

**Signal peptide:**

amino acids 1-29

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GAGGATTTGCACACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT  
GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGG**ATGAT**GGTGGCCCTT  
CGAGGAGCTTCTGCATTGCTGGTTCTGTTCCCTTGCAGCTTTTCTGCCCCCGCCGCAGTGTAC  
CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGAGCAAGGGCTGG  
AAAAATGTACCCAAGCAACGAGGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA  
TCTGTTCATGCTGGGAAGATGTCAGACCTACACAAAGTGAGTACAAGAGTGCAGTGGGTAACTT  
GGCACTGAGAGTTGAACGTGCCCAACGGGAGATTGACTACATAACAATACCTTCGAGAGGCTG  
ACGAGTGCATCGTATCAGAGGACAAGACACTGGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA  
GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC  
TTTGAATAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA  
TCTGATCCAAAGGTGTACTTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAC  
ATACGGGCATTTCATGGAGGATAAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTC  
CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTTCATAACCAAGCAACTT  
CTAATGAGATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA  
GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT  
GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCA  
CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTTCATGGGATACCCCATGCAGAAGCCAG  
GATGCTGAAGCCTCATTCCTCTTGTTGGGGTTCTCTATGTTGGTCTACAGTACTGGGGGCCA  
GGGCCCTCATCGCATCACCTGCATCTATGATCCAATGGGCATATCAGTGAGGAGGACTTGC  
CCAACCTTGTTCTTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCCAGAGAT  
AAGCAGCTCTATGCCTGGAATGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAA  
GCTGCCTCTGAAG**TAA**TGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT  
TACAGGACAGTGAGGCTATAGCCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG  
AGTGTGTAGAAGTGGAATAACGTATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTC  
CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCCAA  
CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTTTTACT  
GCTCCCCAGCATTTACTGTAACCTCTGCCATCTTCCCTCCCACAATAGAGTTGTATGCCAGC  
CCCTAATATTCACCACTGGCTTTTCTCCTCCCTGGCCCTTTGCTGAAGCTCTTCCCTCTTTT  
CAAATGTCTATTGATATTCTCCCATTTTCACTGGCCCAACTAAAATACTATTAATATTTCTTT  
CTTTTCTTTTCTTTTTTTTTGAGACAAGGTCTCACTATGTTGCCCAGGCTGGTCTCAAACCTCC  
AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC  
CACACCTGGCTTAAAATACTATTTCTTATTGAGGTTTAACCTCTATTTCCCTTAGCCCTGTC  
CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAATATTAACATTTGAATATCGCTTT  
CCAGGTGTGGAGTGTGTCACATCATTGAATTCTCGTTTCACCTTTGTGAAACATGCACAAG  
TCTTTACAGCTGTCATTCTAGAGTTTAGGTGAGTAACACAATTACAAAGTGAAAGATACAGC  
TAGAAAATACTACAAATCCCATAGTTTTTCCATTGCCCCAAGGAAGCATCAAATACGTATGTT  
TGTTACCTACTCTTATAGTCAATGCGTTCATCGTTTCAGCCCTAAAAATAATAGTCTGTCCC  
TTTAGCCAGTTTTTCATGTCTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATTCCTCC  
AGAAAACCAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTTGCTTGTGCTGTCTCTGT  
TTCTCTCTTTCTGCTTTAAATTCAATAAAAAGTGACACTGAGCAAAAAAAAAAAAAAA

**FIGURE 262**

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE  
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL  
QEAEKKKIRTLNASCDNMLMGIKSLKIVKKMMDTHGSMKDAVYNPKVYLLIGSRNNTV  
WEFANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED  
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGLGVEHSWDT  
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH  
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

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**FIGURE 264**

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK  
QYQIRIRKEKPQQHNFTHRLLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ  
REHRSMRANVELDHATLVRFSPPDCRAFIWVLANGDTLRVFKMTKREDGGYTFTATPEDFPKK  
HKAPVIDIGIANTGKFIMTASSDTTVLIWLSLKGQVLSTINTNQMNNTAAVSPCGRFVASC  
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV  
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH  
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQRLQQQLTQ  
AQETLKSLGALKK

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

**Beta-transducin family Trp-Asp repeat protein.**

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

**FIGURE 265**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG  
CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC  
TCCTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGT  
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT  
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA  
AGCACACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC  
CGCTGCTCCATGGACTTGAAGAACATCAATTTTTTAGGCGCTTGCCTGGTCTCAGGATACCCA  
CCATCCTTTTCCTGAGCACAGCCTGGATTTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC  
TCTCCCAGTCCCTACACTGACTACCCTGATCTCTTGTCTAGTACGCACATATGCACACAG  
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG  
CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA  
AATGGCAGAAAGGACATTCCCCCTCCCCTCCCAGGTGACCTGCTCTCTTTCCTGGGCCCTG  
CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCCTGGGCACAGGCTCTTGGGT  
GCATTGCTCAGAGTCCCAGGTCTTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGG  
ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTTAGACCACAGAC  
TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA  
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA  
CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT  
TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAA  
TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTTCCTTAAACAACCTCCTTTCCA  
AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG  
TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTAGACCAGGGAGG  
CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

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**FIGURE 266**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAI SLWLRGLRMCTPLGREGEECHP  
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

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**FIGURE 267**

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCTTTC  
CTCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC  
TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG  
CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA  
GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT  
CCTCTGTGCGAGAGGAAGCTGCGGATCTGTCCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG  
TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT  
TTCAAAGGAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT  
GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTTCCGAGCCTGGAACGGAG  
GCTTCTCTGGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCTGTTGGGATCA  
GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT  
TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAATGAT  
TGTGTGAAACTGCCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATT  
GTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTA  
TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA  
CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAAA  
TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG  
TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC  
TCTACTAAAAATACAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG  
GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA  
CACCCTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

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**FIGURE 268**

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR  
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF  
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGLGGVFV  
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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**FIGURE 269**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG  
GGCCAGGTGCCCCGTCGCAGGTGCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA  
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTG  
CTTCTGGCGCTGGGCCTGCCGTTCTTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA  
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG  
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGCTGCCTTG  
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG  
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG  
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCC  
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG  
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG  
GCTATTTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

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**FIGURE 270**

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV  
VFSLLAALLLAVGLALLVRKLRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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**FIGURE 271**

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT  
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTG  
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT  
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC  
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA  
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG  
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA  
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT  
TTATTAATTTTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA  
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAA  
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA  
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

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**FIGURE 272**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK  
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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GCCAGGAATAACTAGAGAGGAGGAACA**ATCGGGGTTATTCAGAGGTTTTGTTTTCTCTTAGTTCT**  
GTGCCCTGCTGCACCAGTCAAATACTTCCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATA  
TTGTCAATTGTTATAGATCCTAGTGTGCCAGAAAGATGAAAAAATAATGAACAAATAGAGGAT  
ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTCAAAA  
TGTATCTATATTAATTCCTGAGAATTTGGAAGGAAATCCTCAGTACAAAAGGCCAAACATG  
AAAACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCA  
TACACCAAGCAGTTCACAGAATGTGGAGAGAAAGGCCAATACATTCACCTTCACCCCTGACCT  
TCTACTTGGAAAAAAACAAAATGAATATGGACCACCAGGCCAACTGTTTGTCCATGAGTGGG  
CTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATGACGCTTTCTACCGTGCTAAG  
TCAAAAAAATAATCGAAGCAACAAAGGTGTTCCGCAAGGTATCTCTGGTAGAAATAGAGTTTATAA  
GTGTCAAGGAGGCAGCTGCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACGTGTATG  
GAAAAGATTGTCAATTCTTTCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATG  
CAAAGTATTGATTCTGTTGTTGAATTTTTGTAACGAAAAAACCCATAATCAAGAAGCTCCAAG  
CTTACAAAACATAAAGTGCATTTTAGAAGTACATGGGAGGTGATTAGCAATTCCTGAGGATT  
TTAAAAACACCATAACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATGTTGCTGAAGATC  
AGTCAAAGAATTGTGTGCTTAGTTCCTTGATAAGTCTGGAAGCATGGGGGGTAAGGACCGCT  
AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGG  
TGGGGATGGTTCACCTTTGATAGTACTGCCACTATTGTAAATAAGCTAATCCAAATAAAAGC  
AGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAACCTCCAT  
CTGCTCTGGAATTAATATGCAATTTCCAGGTGATTGGAGAGCTACATTTCCCAACTCGATGGAT  
CCGAAGTACTGCTGCTGACTGATGGGGAGGATAAACACTGCAAGTTCCTGTATTGATGAAGTG  
AAACAAAGTGGGGCCATTGTTTCATTTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAT  
AGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATTGTTTCTCAGATGAAGCTCAGAACAATG  
GCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACCTGATCTCTCCAGAAGTCCCTT  
CAGCTCGAAAGTAAGGGATTAACTGAATAGTAATGCCTGGATGAACGACACTGTCATAAT  
TGATAGTACAGTGGGAAAGGACACGTTCTTTCTCATCACATGGAACAGTCTGCCTCCAGTA  
TTTTCTCTCTGGGATCCCAGTGGAAACAATAATGGAAAATTTACAGTGGATGCAACTTCCAAA  
ATGGCCTATCTCAGTATTCAGGAAGTCCAAAGTGGGCACTTGGGCATACAATCTTCAAGC  
CAAAGCGAACCAGAAACATTAACATTATACAGTAACCTCTCGAGCAGCAAATTTCTTCTGTG  
CTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTCCTCCAGCCCAATGATT  
GTTTACGCAGAAATTTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTTCAT  
TGAATCACAGAATGGACATACAGAAAGTTTTGGAACTTTTTGATAATGGTGACGGCTGATT  
CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATACAGAAAATGGCAGATAT  
AGCTTAAAAGTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTACGGCCTCCACT  
GAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATGAAGCAAACCCGCCAA  
GACCTGAAATTGATGAGGATACTCAGACCACCTTGGAGGATTTACGCCGAACAGCATCCGGA  
GGTGCAATTTGTGGTATCAACAAGTCCCAAGCCTTCCCTTGCTTGACCAATACCCCAAGTCA  
AATCACAGACCTTGATGCCACAGTTCATGAGGATAAGATTATTTCTTACATGGACAGCACCAG  
GAGATAATTTTGATGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTT  
GATCTAAGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTCCACCAAGGA  
GGCCAACCTCCAAGGAAAGCTTTGCATTTAAACCAGAAAAATCTCAGAAGAAAATGCAACCT  
ACATATTTTATGCCATTAAAAGTATAGATAAAAAGCAATTTGACATCAAAGTATCCAACATT  
GCACAAGTAACCTTTGTTTATCCCTCAAGCAAATCCTGATGACATTGATCCTACACCTACTCC  
TACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTTCTACGCTGGTAT  
TGTCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAGTACCACCATT**TGA**ACCTTA  
ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGGTTTTAAAAAACAAAACAAATGTAAGT  
AAAGGATATTTCTGAATCTTAAATTTATCCCTCATGCCATGTGATCATAAATCATATAAATAAT  
TTAAGATGTGCGAAAGGATACTTTGATTAAATAAAAAACACTCATGGATATGTAAAAACTGT  
CAAGATTAAAAATTTAATAGTTTTCATTTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAAC  
AAAGATCCTTTTTTCACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTTTCTGAAAT  
GATATTTCAAATTTGCATCAAGAAATTTAAATCATCTATCTGAGTAGTCAAATACAAGTAAA  
GGAGAGCAAATAAACACATTTGGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA  
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

**FIGURE 274**

MGLFRGFVFLVLCLLHQSNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTASTY  
LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC  
GEKGEYIHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR  
CSAGISGRNRVYKCGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE  
FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLV  
LDKSGSMGGKDRLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM  
AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDEDNTASSCIDEVKQSGAIVH  
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT  
LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG  
TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG  
YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYSLKVBRAHG  
GANTARLKLRLPPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTLEDFSRASGGAFVVSQV  
PSLPLPDQYPPSQITDLDATVHEDKIILTWAPGDNFDVGKVQRYIIRISASILDLRDSFDD  
ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQAQVTLFIP  
QANPDDIDPTPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

**FIGURE 275**

CTCCTTAGGTGGAAACCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCG  
 GGCAGGGGTGACAAACAGGTGTATCTTTTTGATCTCGTGTGTGGCTGCCTTCCTATTTCAAGGAAAG  
 ACGCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACC  
 CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTT  
 GTGGTTGGAGGAGAGAAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGA  
 GGGTGGACCAAGAAGAAAGGAAAGGTCCCCCTCTTGTCTGTTGGCTGCACATCAGGAAGGCTGTGATGGG  
 AATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAAAA  
 GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATG  
 CAAGCAGCTCCGGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGG  
 GCCCCGGCTTTGAGGGATGCCACCGGTTCTGGAGCGATGGCTGATTCTGAATGATGATGGTTCCGC  
 GGGGGCTGCTTGCCTGGATTTCCTGGGTGGTGGTTTGTCTGGTGTCTCTGTGTGCTATCTCTGT  
 CCTGTACATGTTGGCCTGCACCCCAAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGCCAACAGC  
 CCCACGGGGAAGGAGGGGTACCAGGCCGCTCCTCAGGAGTGGGAGGAGCAGCACCAGCACTACGTGA  
 GCAGCTGAAGCGGAGATCGCACAGCTCAAGGAGGAGTGCAGGAGAGGAGTGGTGGTGGAAAGCCATT  
 TGGGCAGTACCAAGCCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAG  
 GCGGACCTCCTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGG  
 CCACAGAGTATGCAGCAGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG  
 CCTTACCCGCCACCCGAGGAGAAGCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCCATT  
 GAATCAGCCTTGGAGACCCTGAACAATCCTGCAGAGAACAGCCCCAATCACCGTCTTACACGGCCT  
 CTGATTTTCATAGAAGGGATCTACCGAACAGAAAAGGGACAAAGGGACATTGTATGAGCTACCTTCAA  
 AGGGGACCACAAACAGCAATTCAAACGGCTCATCTTATTTGACCATTACAGCCCCATCATGAAAGTG  
 AAAAAATGAAAAGCTCAACATGGCCAACACGCTTATCAATGTTATCTGCTCTAGCAAAAAGGGTGG  
 ACAAGTTCGGCAGTTTCATGCAGAAATTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCT  
 CACTGTTGTTTACTTTGGGAAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAA  
 GCTGCCAATTTCAGGAACCTTACCTTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGGACTTG  
 ATGTTGGAGCCCCGCTTCTGGAAGGGAAGCAACGCTCCTTCTCTTTCTGTGATGTGGACATCTACT  
 CACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAGGTATTTTATCCAGTT  
 CTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAAACAGC  
 AGCTGGTCATAAAGAAGGAAACTGGATTTTTGGAGAGACTTTGGATTGGGATGACGTGTGATATCG  
 GTCAGACTTCATCAATATAGGTGGGTTTGTATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC  
 CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCCTGTGCGAGGACTCTTCCACC  
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAA  
 GGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTGGTGTTCAGGCACGAGATAGAGGCTCAC  
 CTTGCAAAACAGAAACAGAAAGACAAGTAGCAAAAAAACATGAAGTCCCAGAGAAGGATTGTGGGAGA  
 CACTTTTTCTTTCTTTTGAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAAGGACG  
 ACAAAAGAATTGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTGGGCTTTTTAC  
 AACAGAAATCAAAATCTCCGCTTTGCCTGCAAAAGTAACCCAGTTGCACCCGTGCAAGTGTCTGACA  
 AAGGCAGAATGCTTGTGAGATTATAAGCCTAATGGTGTGGAGGTTTGTATGGTGTTTACAATACACT  
 GAGACCTGTTGTTTTGTGTGCTCATTGAAATATTCATGATTTAAGAGCAGTTTTGTAAAAAATTCAT  
 TAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGAGCCTATCAGCAGGGCTCTAGTTTCTAGG  
 AATGCTAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATTATGATACTAGTGAGTACATTAAGTA  
 AAATAAAATGGACCAGAAAAGAAAAGAAACCATAAATATCGTGTCAATTTTTCCCCAAGATTAACCA  
 AAAATAATCTGCTTATCTTTTTGGTTGTCTTTTAACTGTCTCCGTTTTTTTTCTTTTATTTAAAAAT  
 GCACTTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTATTAATTACCACTTTGCAAGCCTTACAAGAGA  
 GCACAAGTTGGCCTACATTTTTTATATTTTTTAAGAAGATACTTTGAGATGCATTATGAGAAGTTTCA  
 GTTCAAAGCATCAAATTGATGCCATATCCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAAT  
 GTCAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGACGTACAGATACTTTCTCTGAA  
 GAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGACACTTTCTGCTTTACAGAA  
 AAGGAAACTCATTACAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCACATTTTCTCCTCA  
 GAAGTAGGGACCGCTTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACAATCTCT  
 TTTCAAAACAGGGTGCTCCTCCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAAATATATATAT  
 ATATATATATATTGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTGTGCTACAT  
 GTTATCCACCCCAGGCCAGGTGGAAGTAACTGAATTATTTTTTAAATTAAGCAGTTCTACTCAATCA  
 CCAAGATGCTTCTGAAAATTGCATTTTATTACCATTTCAAACATTTTTTTAAAAATAAATACAGTTA  
 ACATAGAGTGGTTTCTTCATTCATGTGAAAATTATTAGCCAGCACCAGATGCATGAGCTAATTATCT  
 CTTTGGTCTTCTGTTTGTCTCAGATTAATCATGTTTAAAAAGCTTCAAGAACCTTACAGAAC  
 TGTTGGTGTGTTAAAAAATGCATTGTATTGATTTGTACTGGTAGTTTATGAAATTTAATTAACAC  
 AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

**FIGURE 276**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ  
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL  
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIES  
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP  
MKVKNEKLNMAN TLIN VIVPLAKRVDKFRQFMQNFREMCIEQDGRVH LTVVYFGKEEINEVK  
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLN TCR  
LNTQPGKKVFYPVLF SQYNPGIIYGHHD AVPPLEQQLV IKKETGFWRDFGFGMTCQYRSDFI  
NIGGFDL DIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTP EQYKMCMQS  
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

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**FIGURE 277**

GAAAGAATGTTGTGGCTGCTCTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACC  
AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT  
ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA  
GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT  
ATCATTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC  
AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCT  
CTGGAATTTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG  
GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT  
CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT  
AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG  
GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT  
TGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA  
CCAAGAGCAGATCATATATTTTGTTCACCATTCTTCTTTTGTAAATAAATTTTGAATGTGCT  
TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC  
TCAAAATATTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG  
TAGTTATTGATTTAAGCATTTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTC  
AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT  
TGAAAATGGATCCTTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG  
TGAGAAGTAATTATTGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATT  
TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC  
AATTCTATTTGTTGACCATTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG  
TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 278**

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVÁF'SMRKVP  
NREATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLE  
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLLSGIWQRRRKNKEPSEVDDAEDKC  
ENMITIENGIPSDPLDMKGGILMMPS

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**FIGURE 279**

AACTCAAACCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG  
GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTCCTC**ATGT**  
ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG  
CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC  
TCGGTTAAAATGCACTTTCTCCAGCTTTGCCCCTGTGGGTGATGCTCTAACAGTGACCTGGA  
ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC  
CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGCTTGGGATGGGAATCCTGAGCGGTACGA  
TGCCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA  
AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA  
CGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT  
AATAGTAATTGTAGTGGTCCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC  
ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT  
GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA  
GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT  
TTTCCAACCAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC  
AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA  
GTGTAAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTTGCCCTTAA  
GACACTACTTACAGTGTTATGACTTGTATACATATATTGGTATCAAAGGGGATAAAAGCC  
AATTTGTCTGTTACATTTCTTTTACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA  
ATGTGTTTACTCTCTTTTCTTCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTG  
TTTCTGATTAACAGTAAATCCTAAATTCAAACCTGTAAATGACATTTTTATTTTTATGTCTC  
TCCTTAACATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATT  
TTTGTCG

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**FIGURE 280**

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT  
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ  
VKNPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLFFQHYRKKRWAER  
AHKVVEIKSKEEERLNQEKVSVYLEDTD

0997444544  
0997444544

**FIGURE 281**

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCA**CCATGA**AGTTCTTAGCAGTCCTGGT  
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG  
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT  
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG  
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCC**T**  
**G**AGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAAC**TATTCATGCTTCCTGTGAT**TC  
ATCCA**ACTACTTACCTTG**CCTACGATATCC**CCCTTATCTCTAATCAGTTTATTTTCTTTCAA**  
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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**FIGURE 282**

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTTAT  
TAASTTARKDIPVLPKWVGDL PN GRVCP

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**FIGURE 283**

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC  
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC  
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA  
GTGTCCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC  
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG  
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG  
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT  
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTTAAAACCACAGGCTGG  
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA  
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTTACCACATTAGCAATTAAAACTGAGAAAT  
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT  
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA  
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG  
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT  
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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**FIGURE 284**

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG  
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCCWPVGVARGGALCQ



**FIGURE 285**

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA  
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG  
GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA  
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC  
CGGGGCCGGGATGCAGCCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA  
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCCAGGCACAGA  
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT  
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC  
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC  
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCCTGAATCTGCCTGGATGGAAGTGA  
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG  
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC  
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA  
CCCTTTTCATGCCTACACACCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 286**

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK  
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK  
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ  
IQERLHTAALPA

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**FIGURE 287**

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT  
CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA  
AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC  
TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC  
TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG  
AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACTCCGACGAAATCAACGCC  
CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA  
CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGG  
ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACGTGTGTCCTGTTCTCCCAATCAGCTCAG  
GGCAAGTGGAGTGATGAGGCCTGTGCGCAGCAGCAAGAGATACATATGCGAGTTACCATCCC  
TAAATTAGGTCTTTCTCCAATGTGTCCTCCAAGCAAGATTCATCATAACTTATAGGTTCATGA  
TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAAAAAATTGCAACACAAGATCAAT  
GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT  
TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT  
AAACAGACTAAAATCTTTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA  
AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT  
TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT  
GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACC  
TTGTCAGCCCATACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT  
GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC  
TACCCTTTTTTTTGGAAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT  
CAATTTTCATTCCCACCATTCGATTACAACCTCTAACTTAAATGGGTAACCCTAAGGCATAT  
CAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT  
AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTTACATTT  
TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT  
TGGAAGCTGAAAACCTGAATTTAAAGAATGCTATCTTGGAATTTGCATACGTCTGTGCAATT  
TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT  
TAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAAAGCAAACAATTTT  
AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT  
CCCCTTTGCAAACCTTAACTACACATGCTTGGAATTAAGTTTTAGCTGTTTTTCATTGCTCA  
ATAATAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 288**

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHKKRRVRDKDGLKTQIEKLWT  
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ  
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSQAQ GK  
WSDEACRSSKRYICEFTIPK

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**FIGURE 289**

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCTCCGCGCGC  
CCCGAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA  
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTG  
GAGTCGGCGGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCT  
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT  
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG  
GCCCTGACAGTGTTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC  
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCT  
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 290**

MKLAALLGLCVALSCSSAAAFVGSAPVAPVAALESAAEAGAGTLANPLGTINPLKLLLS  
SLGIPVNHIEGSQKCVAELGPQAVGAVKALKALLGALTVFG

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TGAAGGACTTTTCCAGGACGCCAAGGCCACACACTGGAAGTCTTGACAGCTGAAGGGAGGCACT  
CCTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTG  
GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCCAGCCCC  
TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG  
CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT  
GCCAAGGAGACTTCAAACCTTCGGATTACGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG  
CAACATGGTCTTCTCTCCATTTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCA  
CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGACAGGCCCTGAAGCCCACCAAG  
CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAAC  
GGGCTCTCACAGGGGAGTTTTTGCCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT  
TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTATGAATTTTCGCAATGCCTCA  
CAGGCCAAAAGGCTCATGAATCATTACATTAACAAGAGACTCGGGGGAAAATTCCCAAAC  
GTTTGATGAGATTAATCCTGAAACCAAATTAATCTTGTTGATTACATCTTGTTCAAAGGGA  
AATGGTTGACCCCATTTGACCCTGTCTTCACCGAAGTCGACACTTTCACCTGGACAAGTAC  
AAGACCATTAAAGGTGCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA  
TTTTCGTTGTGATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA  
TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA  
TGGCTCAGAAACATGAAAACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCA  
GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCTTTG  
CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA  
ACAGTGATTGAAGTTGATGAAAAGGGCACTGAGGCAGTGGCAGGAATCTTGTCAGAAATTAC  
TGCTTATTCCATGCCTCCTGTCATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG  
AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTAT**TAA**TTCAG  
ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACAGGA  
TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTTGTCTTAACTAGTTTtagggTGTCTC  
AAATAAATACAGTAGTCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC  
CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTTACACATACATACCTATGAT  
AAAGTTTAAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAAGTAAAA  
TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA  
CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA  
CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCACTACTCAGAATGGCATGC  
TGCTTAAGACTTTTtagattGTTTATTTCTGGAATTTTTTCATTTAATGTTTTTGGACCATGGT  
TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA  
GCATTAAATTGATACATATTTTTTTAAAAAAAAAAAAAAAAAAAAA

**FIGURE 292**

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E  
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I  
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F  
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P  
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L  
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A  
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F  
L G R V V N P T L L

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**FIGURE 293**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAG  
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG  
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG  
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCC  
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA  
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCCTGAGTCCC  
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC  
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA  
TCTACCACCCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGG  
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA  
AAAAAAAAAAAAAAAAA

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**FIGURE 294**

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL  
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE  
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

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**FIGURE 295**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG  
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC  
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA  
TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC  
TAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT  
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG  
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC  
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGGCGGCCACGAGCG  
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG  
CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC  
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT  
ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC  
GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATT  
TGTTCAAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG  
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT  
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACTCATGTTGGTTA  
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG  
GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTACCCA  
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

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**FIGURE 296**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN  
GVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG  
SAEAATSDDYKNPGYYDIQAKDLGIWHVFNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI  
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRVFNNERAAN  
ALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL  
FYR

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**FIGURE 297**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC  
CACGAGGCTGCCGCATCCTGCCCTCGGAACA**ATG**GGACTCGGCGCGCGAGGTGCTTGGGCCG  
CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC  
ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC  
AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC  
CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG  
GCATCTAATAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC  
TACACCCAAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG  
TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT  
TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC  
GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC  
GGTATCGAACCATAGATGAACATGATGCCATCATT**TAAG**GAAATCCATGGACCAAGGATGGA  
ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCT  
CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA  
AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT  
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCT  
GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA  
TGCCATCTGGGCATACAAATAAGAAGTTTGTCACAGCACTCAGGATTTTGGGTATCTTTTGT  
AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA  
CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG  
TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

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**FIGURE 298**

MGLGARGAWAALLLGTLLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVP  
SDH  
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSV  
SQN  
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSI  
LYIG  
CKMYYSRRGIRYRTIDEHDAII

**FIGURE 299**

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCCGAGCCGGGAGCCGG  
TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCG**ATG**GCGACCCTGTGGGGAGGC  
CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCGGTGCTGCTGCTGGC  
GCAGCTGTCAGACGCCCAAGAATTTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCT  
ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT  
CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA  
ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA  
TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG  
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT  
TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG  
AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG  
CATGTTGTCCTCAGC**TAA**TTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA  
CTGGAAGAAGTACTGAGTGGGTTTTGCTGGGTTTTCAATTTTAATACCTTGTTGATTTACCAACT  
GTTGCTGGAAGATTCAAAAGTGAAGCAAAAAGTCTGCTTGATTTTTTTTTCTTGTTAACGTA  
ATAATAGAGACATTTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTG  
TGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA  
AGCACTCTCTTTTTTACCACATAGTTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG  
TTGTTGTTGTTTTTTTTGTTTGTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT  
AACAAGTTTTTTCAAGTCACCTTTACTAAACAAACTTTTTGTAAATAGACCTTACCTTCTATTT  
TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG  
ACTTTTGCAGTACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGAT  
CTAAAATGCCTGGTGGCTTTTCACAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG  
CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG  
GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGAACACT  
TGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTG  
TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACT  
AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT  
TCTTCCTATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA

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**FIGURE 300**

MATLWGGLRLGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS  
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVYLT  
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLRSSRANVLNKVEYAQQRWKLQVQEQ  
RKSVFDRHVLS

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**FIGURE 301**

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT  
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCCCAAGGCCTTCCTGTCCCGCGGGAAGCGG  
CAGGAGCCGCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA  
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG  
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG  
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTTATATATACTGTACATTCTATT  
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA  
TCATTGTCTACATTAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA  
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTTCAGTTTCACATAAGAATG  
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTT  
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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**FIGURE 302**

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGREFPPMMHHHQAPSDGQT  
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIPIYGFIFLYILYILFKVSRILI  
ILHQ

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**FIGURE 303**

CGGCTCGAGTGCAGCTGTGGGGAGATTTAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT  
GGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTAC  
TGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTG  
GGTGATTAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT  
AGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA  
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGC  
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA  
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG  
AGGAGCCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAGATGGGATGTGTTTTCCAG  
AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA  
GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGG  
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCCATCATG  
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT  
GGTGTTCAGAAAACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCC  
CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC  
TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA  
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG  
AAAAACCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA  
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA  
CCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG  
GAATGCCAAAAACACAGCAAGCCTTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG  
TGGAGACTCTCTCCTGTGTGTGTCTGGGCCACTCTACCAGTGATTTAGACTCCCGCTCTC  
CCAGCTGTCCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG  
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC  
CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTT  
GGATCAGACCCTCCTGTGGGCAGGGTTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATA  
AAAACCAACCCAAATCAA

**FIGURE 304**

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG  
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTyceIRLKGES  
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY  
HKLRMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV  
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLLPVLILIVKKTCGNKSSVNSTV  
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSP IIVREVIEEEEPSEKSEATYMTMHPVWPSLR  
SDRNN SLEKKSGGGMPKTQQAF

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**FIGURE 305**

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG  
GTTCTACCCTACTAAAGACAGGAAGATCATAACTGACAGATACTGAAATTGTAAGAGTTGG  
AAACTACATTTTGC AAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA  
GGATGAAGATGGATACATCACCTTAAATATTA AAACTCGGAAACCAGCTCTCGTCTCCGTTG  
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG  
ATGGTTGTCTGGGCTGGTGGCTCTGGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGA  
TGAGAATGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG  
TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCCTGTGACACAAAC  
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG  
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG  
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCTGGATTATCTCGCCAGAAGTCGAAT  
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA  
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG  
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT  
**TAA**TGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT  
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

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**FIGURE 306**

MQDEDGYITLNIKTRKPALVSVGPASSSSWVRVMALILLILCVGMVVGLVALGIWSVMQRNYL  
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLWE  
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL  
EDGKGNMNCAYFHNGKMHPTFCENKHLYLMCERKAGMTKVDQLP

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**FIGURE 307**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGCGATCCCGG  
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCCGCGCGGGAGCCGGACCGC  
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAA  
GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG  
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAGAAGCGGTGGTGGTGGG  
CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG  
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC  
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG  
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC  
ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACT  
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT  
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTCACACCTGAGTGCA  
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG  
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA  
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT  
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC  
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC  
**G****TAG**CCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT  
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG  
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

**FIGURE 308**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLVFSRVKLFSGSKRRRRRP  
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDDSTYTLFNLI PVGLRVVAIQGVQTKLYLA  
MNSEGILYTSSELFTECKFKESVFENYYVTYSSMIYRQQSGRGWYLGLNKEGEIMKGNHVK  
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMSHNEST

**N-glycosylation site.**

amino acids 242-246

**Glycosaminoglycan attachment site.**

amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site.**

amino acids 93-100

**N-myristoylation site.**

amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop).**

amino acids 231-239

**HBGF/FGF family proteins**

amino acids 78-94, 102-153



**FIGURE 309**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG  
ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG  
CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCT  
CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCTTCTGACATTGGCAGTG  
CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC  
AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA  
ACCACGTCTTGGAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG  
GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG  
AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCT  
GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG  
CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAG  
CGCGCTCCGGGCGCCTGCCGTTTTGGGGGTGTCTCCTCCCGGGGCGCT~~ATG~~GCGGCGCTGGC  
CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCCGGGGGCAGCCGGCCGGTGTCCG  
CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG  
CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCCGCGCGGCGGACCGCGGCCCCGAGCCTCA  
GCTCAAAGGCATCGTCACCAAACTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG  
ACGGAAGCATCCAGGGCACCCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT  
GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC  
TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTCGCTTTAAGGAGTGTGTCT  
TTGAGAATTACTACGTCCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC  
TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAA  
GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC  
ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCC~~TGA~~AATGTAGTCCCTGGACTG  
GAGGTTCCCTGCACTCCCAGTGAGCCAGCCACCACCACAACCTGT

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**FIGURE 310**

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR  
GPEPQLKGIVTKLFCRQGFYQLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY  
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR  
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

**Tyrosine kinase phosphorylation site:**

amino acids 199-207

**N-myristoylation sites:**

amino acids 54-60, 89-95, 131-137

**HBGF/FGF family signature:**

amino acids 131-155

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**ATG**GCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG  
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGGCTCTGCAACG  
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG  
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT  
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT  
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT  
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT  
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG  
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA  
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG  
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA  
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACAT**TAG**

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## **FIGURE 312**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDPRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR  
RQDPQLKGIVTRLYCRQGYLQMHDPGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY  
IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR  
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

### **N-glycosylation site.**

amino acids 100-104, 242-246

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 28-32, 29-33

### **Tyrosine kinase phosphorylation site.**

amino acids 199-207

### **N-myristoylation site.**

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

### **HBGF/FGF family proteins.**

amino acids 104-155, 171-198

**FIGURE 313**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAT  
 GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA  
 ACGAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG  
 AAATAAACCAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTCCCC  
 CTCCCCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACAAAAGAAAAAGTATGTTCAATTT  
 TTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA  
 AGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGC  
 AAAGAAATTTAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCA  
 CAGTTGGATTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT  
 TTTTAAATTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACCTGGATTTCCATCT  
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACCAGATAAATTATGAATG  
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCT  
 GCTTGTGGTGTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCAGGGCTCAGACCTGCCCTTCTGTGT  
 GCTCCTGCAGCAACCAGTTGAGCAAGGTGATTTGTGTTTCGGAACCTGCGTGAGGTTCCGGATGGCATCTCC  
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAG  
 GCACCTTGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTCAATGGTCTGGCGA  
 ACCTCAACACTCTGGAACCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAA  
 CTGAAGGAGCTCTGGTTGCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTT  
 GCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTTATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAAC  
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAG  
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAAAC  
 GTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCA  
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT  
 TTACATCACAACCTTTGGAACGTAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC  
 GAACACAGCTTGTTGTGCCCCGGTGTAACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA  
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT  
 GAGCTGAAATGTGCGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA  
 TGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTACAAATGTAAGTGTGCAAGATA  
 CAGGCATGTACACATGTATGGTGAGTAATTCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCA  
 GCAACCACTACTCCTTTCTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG  
 GACCACAGATAACAATGTGGGTCCCCTCCAGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACAC  
 CACAGAGCACAAGGTGACAGAGAAAACCTTCACCATCCAGTGACTGATATAACAGTGGGATCCCAGGAATT  
 GATGAGGTGATGAAGACTACCAAATCATCATTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT  
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAAGGACTGTTGAAATTA  
 TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAG  
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTCATAC  
 CAGTTCAGTGATGAACCGTTATTGATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATCTAAACAA  
 TTTACAGAGTTACAAAAACAAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAA  
 ATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAACAAAAAGAAATTTATTTATTAATAATTCTATTG  
 TGATCTAAAGCAGACAAAAA

**FIGURE 314**

MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRIS  
YISEGAFEGLSNRLRYNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLVTEGMAAE  
LKCRASLSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVNSVGN  
TTASATLVNTAATTTTFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,  
434-438, 442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT  
 GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTGCGGA  
 GGCGCCCGGCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC  
 GGG**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA  
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC  
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
 AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGACAGATTGAACCTCTGAAGC  
 CCAGTGATGAGGGCCGTTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT  
 GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
 AGAAGGAAGTGACCTGACTTTGACAGTGTGAGTCATCCTCTGGCACAGAGCCATTGTGTATT  
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAATCTAGGATT  
 GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA  
 CCAGTGACACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAAGTGTACAGT  
 ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
 ATTTTCCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
 GAGACCTAATGAAATTGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT  
 CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACTCGCTCCACAGCAAAT  
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCCGAGCCAGGGCTGGCCAC  
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAAGTCCACCATG  
 CTAATCTGACCAAGCAGAAACCACACCCAGCATGATCCCAGCCAGAGCAGAGCCTTCCAA  
 ACGGTCT**GAA**ATTACAATGGACTTGACTCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC  
 TTCTCGTCAATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
 GTGAGCATTGCACGGAACAGATTGAGATGAGCATTTTCTTATACAATACCAAACAAGCAAA  
 AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
 AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
 AGGTGAATATACCTAAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAAATT  
 TTCAAGAGGAAATGGGATGCTGTTTGTAATTTTCTATGCATTTCTGCAAACCTTATTGGATT  
 ATTAGTTATTGAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
 TGAGCTAACCACTTCTAAGAAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
 TTCATTTGTGATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC  
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCATGATGTT  
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCTCAAAT  
 CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT  
 TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAGGGATCTAGGAATGCTGAAAGATTGA  
 CCAACATACCATTTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG  
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
 TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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## **FIGURE 316**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLVSYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSEGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSRSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251



CCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCGCCTACCTGCAGCGCGCGCCACGGCACGGCAGCCCA  
CCATGGCGCTCCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTCCGCCAGAAGTTTGAGTATCACTACT  
CCTGAAGAGATGATTGAAAAAGCCAAAGGGGAAACTGCCTATCTGCCATGCAAATTTACGCTTAGTCCCGAAGA  
CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTTAT  
ATTCTGGAGACAAATTTATGATGACTACTACTCCAGATCTGAAAGGCCGAGTACATTTTACGAGTAAATGATCTC  
AAATCTGGTGATGCATCAATAAAGTAAACGAATTTACAACCTGCAGATATTGGCACAATATCAGTGCAAAGTGAA  
AAAGGCTCCTGGTGTTCGAAATAAGAAAGATTTCATCTGGTAGTTCTTGTTAAGCCTTCAGGTGCGAGATGTTACG  
TTGATGGATCTGAAGAAATTGGAAGTGACTTTAAGATAAAATGTGAACCAAAGAAGGTTCACTTCCATTACAG  
TATGAGTGGCAAAAATTGTCTGACTCACAGAAAATGCCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT  
ATCTGTAAAAAATGCCTCTTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC  
AGTGCCTGTTGCGTCTAAACGTTGTCCCTCCTTCAATAAAGCTGGACTAATTCAGGAGCCATTATAGGAAC  
TTGCTTGCTCTAGCGCTCATTTGGTCTTATCATCTTTTGCTGTGTAAGAACGCGCAGAGAAGAAAAATATGAAAA  
GGAAGTTTCATCAGGATATCAGGGAAGATGTGCCACTTCCAAAGAGCCGTACGTCCACTGCCAGAAGCTACATCG  
GCAGTAATCATTCATCCCTGGGGTCCATGTCTCCTTCCAACATGGAAGGATATTCCAAGACTCAGTATAACCAA  
GTACCAAGTGAAGACTTTGAACGCACTCCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAAGTACCCTTACAA  
GACTGATGGAATTACAGTTGTATAAATATGGACTACTGAAGAATCTGAAGTATTGTATTATTTGACTTTATTTT  
AGGCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGAGCAGCTGTAAGAACAC  
ATCATCTTTATGCAATGGCATTTAGACATGTAAGTCAGATGTCAATGCTCAAAATTAGTACGAGCCAAATCTTTGT  
TAAAAAACCTTATGTATAGTGACACTGATAGTTAAAAAGATGTTTTATTATATTTTTCAATAACTACCCTAACAA  
ATTTTTAACTTTTCATATGCATATTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTTCAA  
AGGAAATTTTAAATTTCTTACGTTCTGTTTAATGTTTTGCTATTTAGTTAAATACATTGAAGGGAAATACCCG  
TTCTTTTCCCCTTTTATGCACACAACAGAAACACGCGTTGTGATGCCTCAAACATTTTTTTTATTTGCAACTACA  
TGATTTTCACACAATTCTCTTAAACAACGACATAAAAAATAGATTTCCCTGTATATAATAACTATACATACGCTCCA  
TAAAGTAAATTTCTCAAAGTGCTAGAACAAATCGTCCACTCTACAGTGTCTCGTATCCAACAGAGTTGATGC  
ACAAATATATAAATCATCAAGTCCAAATATTAATAAAGCTTAGGCACCTGACTAAGTTTAAATAAAATTTCTCAAAC  
TATCAATATCTAAAAGTGCATATATTTTTTAAAGAAAGATTATTTCTCAATAACTTCTATAAAAAATAGTTTGTG  
TTTGGCCCATCTAACTTCACTACTATTAGTAAGAAGCTTTTAACTTTTAAATGTGTAGTAAGGTTTATTCTACCTT  
TTTCTCAACATGACACCAACCAATCAAAAACGAAGTTAGTGAGGTGCTAATCATGTGAGGATTAATCCAGTGAT  
TCCGGTCACAATGCATTTCCAGGAGGAGGTACCCATGTCACTGGAATTTGGCGATATGGTTTATTTTTTCTTCCC  
TGATTTGGATAACCAATGGAACAGGAGGAGGATAGTGATTCTGATGGCCATTCCTCGATACATTTCTGGCTT  
TTTTCTGGGCAAAGGTGCCACATTGGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT  
TAAGTTAATTCAAAGGAAAAAATCATCATCTATGTTCCAGATTTCTCATTAAAGACAAAGTTACCCACAACACT  
GAGATCAGATCTAAGTGACACTCCTATTGTGAGGTCTAAATACATTAAAAACCTCATGTGTAATAGGCGTATAA  
TGATAACAGGTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAAACTCAACACAGTACTTCCTAAACAA  
CTTCAACCAAAAAGGACCAAAACATGGAACGAATGGAAGCTTGTAAGGACATGCTTTGTTTAGTCCAGTGGTTT  
CCACAGCTGGGTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAAACATTGGAGCTGGAGGCCATTATCCTT  
AGCAAACCTAATGCAGAAACAGAAAATCAACTACCGCATGTTCTCACTTATAAGTGGGAGGTAATGATAAGAACT  
TATGAACACAAAAGAAGGAAAACAATAGACATTGGAGTCTATTTGAGAGGGGAGGGTGGGAGAAGGAAAAGGAGCA  
GAAAAGATAACTATTGAGTACTGCCTTCACACCTGGGTGATGAAATAATATGTACAACAAATCCCTGTGACACA  
TGTTTACCTATGGAACAAACCTTCATGTGTATCCCTAAACCTAAAATAAAAGTTAAAAAARAAAAA  
AAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA  
AAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA

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## **FIGURE 318**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA  
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK  
APGVANKKIHLLVVLVKPSGARCIVDGSSEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT  
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL  
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM  
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

### **Signal sequence.**

amino acids 1-19

### **Transmembrane domain:**

amino acids 236-257

### **N-glycosylation sites.**

amino acids 106-110, 201-205, 298-302

### **Tyrosine kinase phosphorylation sites.**

amino acids 31-39, 78-85, 262-270

### **N-myristoylation sites.**

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,  
245-251, 296-302

### **Myelin P0 protein.**

amino acids 96-125

**FIGURE 319**

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA  
ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC  
CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC  
CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG  
AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC  
CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTG  
CTTCTCTGGAGCCAGGTATCAGGGGCCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT  
GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG  
CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT  
GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGTTCACAAAA  
CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACA  
TTGTTCTCATCGTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC  
AGTGCACACAGGCGGTTTTCTGCTATTCGGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC  
TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGC  
TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTTGTTCCCTGTGTCATTTCA  
AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT  
TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG  
GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTT  
AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG  
CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG  
TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT  
GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAAGTGAAGTTTCAAGAGCATGAAAATCACACT  
GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAAGGTGCATCTGTTTGAAAAG  
TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT  
TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT  
TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC  
ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA  
CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 320**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGQEFHFGPCQVK  
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH  
HNRTVEVRTLSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL  
TKALGEVDILLTWMQKFYKL

### **Signal sequence:**

amino acids 1-42

### **N-glycosylation sites.**

amino acids 85-89, 99-103, 126-130

AAGGAGCAGCCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC  
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCCACGGTCTCAGGAGATGTCTGATTTT  
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG  
ACACCTTCCCAAATGTCACCTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA  
GATGTGTGCTGCGTGACCAAGAACCCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA  
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA  
TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC  
AATGCCACCAGAGTCATCCATGACAACCTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT  
GTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC  
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCCAAAAGTCTACTGTGGTAT  
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT  
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

**FIGURE 322**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST  
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ  
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

**Signal sequence:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 56-60, 135-139

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation site.**

amino acids 24-30

**Actinin-type actin-binding domain signature 1.**

amino acids 159-169

**FIGURE 323**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG  
AACGCGGCTACAATTAATACATAACCTTATGTATCATAACACATACGATTTAGGTGACACTAT  
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC  
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCCGCCT  
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA  
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC  
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC  
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA  
TGAGCAGAAGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTTTCGAC  
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC  
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC  
CACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTTCAACACC  
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGT  
GCTGAAGCCCCGGGCCCCGGATGACCCCGGCCCGGCCCTCCTGTTACAGGAGCTCCCGAGCG  
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAAC  
ACGCACGCTGGGGGAACGGGCCCCGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCTG  
CTGG

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVD  
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGY  
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRRNEIPLIHFNTPIPRRHTRSAEDDSE  
RDPLNVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA  
KFI

## amino acids 73-124



**FIGURE 325**

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**  
GGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG  
GAGCTCTGCAGGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG  
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG  
ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA  
GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC  
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC  
ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA  
TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA  
CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC  
ACCCCGTACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC  
GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT  
GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG  
GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGA  
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC  
CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC  
ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA  
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGAGGCTCTGGTCA  
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC  
AAAGTCTCAGGAGCAGTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTTC  
CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC  
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCT  
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA  
GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC  
GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTG  
TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC  
CGGGAACCTCCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA  
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCCTAGCCTG  
GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG  
AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC  
CGGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCCAGAGGTGTCTTGGACTCACCTTGG  
CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA  
TTAAAATTCACTCAGTGTGGCCCAAAAAAA

**FIGURE 326**

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL  
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAASGSPEGAGM  
 TTVQTITGSDPEEAI FDTLCTDDSS EEA KTLTMDILT LAHTSTEAKGLSSESSASSDGPHPV  
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTNI  
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL  
 STAGTTESAAPHATVGTPLPNTSATEREVTAPGATTLGALVTVSRNPLEETSALSVETPSY  
 VKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTSRD  
 PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRRLPGRGRPQT

**N-glycosylation sites:**

amino acids 252-256, 445-449, 451-455

**cAMP-and cGMP-dependent protein kinase phosphorylation site.**

amino acids 84-90

**Casein kinase II phosphorylation sites.**

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,  
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,  
 404-408, 414-418, 431-435

**N-myristoylation sites.**

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-  
 320, 349-355, 386-392, 397-403, 449-455

**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

**FIGURE 327**

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCGCGCGGATTGCGCCGGTCCTTCCCGCGG  
GCGCGACAGAGCTGTCCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCCTCTCGACGCCA  
GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAATAAGACCAGAGGGAGGATTAT  
CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAAATGTTCTTCGGGGGAGAAGGGAG  
CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
GCCTCAAAAAGAGTCTAGAAGATGTTGTGATTGACATCCAGTCATCTCTTTCTAAGGGAATC  
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC  
AAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA  
GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA  
AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCC  
TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT  
CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA  
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA  
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
CATAACACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC  
TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACCTTCTC  
AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG  
GCTACAACAGCAGTTCTGACTACCACCTTTGAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
AACCATAACCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCCTA  
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCCTGGGAAGGT  
AGGGAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC  
ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGCTGATAGGCC  
TCGTCTCCTGGGTAGAATCCTTTCCGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT  
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT  
TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG  
TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCTTTTTTTTTTTGGAGACAGAGTCTT  
GCTCTGTTGCCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC  
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG  
GTCTCAAACCTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG  
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG  
GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT  
ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA  
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATTCTTGGTTCCAGATAAAATCAAC  
TGTTTATATCAATTTCTAATGGATTTGCTTTTCTTTTTATATGGATTCCTTTAAACTTATT  
CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

**FIGURE 328**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTRLSASQNCLKKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED  
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP  
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF  
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL  
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFETRAAATLQAMATTAVLTTFQAP  
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV  
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRDLYLINGIYVDI

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321

CTCCACACCGGTGTCCAGGCGCCAGAAATGCGGCTTCTGGTCTGTCTATGGGGTTGCCTGCTGCT  
CCCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAAATCAGCGGGTTTGAAGGGGACACTGTGT  
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA  
ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG  
TCTTTACTGATCTCTCTGTTCTGTTTCCAGGACCCTGCTGTCTCCCTCCCTTCTCCAC  
CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCC  
CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
GCTGAGGCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCATGCAGC  
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCTGGTGCTGCTGAGCCTTCTGTGAGC  
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC  
CCTTCCCAGGGCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA  
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT  
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTCCCGAGGCTCTCCTCTTGATGTTCCA  
GCCTGACCTAGAAGCGTTTGTCTAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
GAGACTGGGACATCCCTGATAGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA  
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC  
CTCATGCCAGTGTGCGACCCCTGCCTTCCCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC  
TGGCGTCCCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTATGAAGAGGAGCATGCT  
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAAGGAAGCCT  
GTGAAAAACGTGATTCCCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
GACTCTGAATTCTAACAATGCCAGTGACTGTGCGACTTGAGTTTGAGGGCCAGTGGGCCTG  
ATGAACGCTCACACCCCTTCAAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC  
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG  
TCCAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG  
TTGCCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCCTTTGGAAAAAATGATGAAGA  
AAACCTTGGCTCCTTCCCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA  
GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA  
GCACAATACTACTATTTTTTTTTCTTTTTTCCATTATTATTGTTTTTTTAAAGACAGAATCTCGTGCT  
GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCCTCCTGGGTTCAAGTGATT  
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT  
TTTGTACTTTTAGTAGAGATGGGGTTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCTGAC  
CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG  
TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCAAGTATGCAAACTTGGAAAG  
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT  
TATTTTCTTTTTGTTGTACTTCTTCCACTCTTTTCTTCTTCCATAATTTGCCGGTGTCTTT  
TTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
ATCACTTTATTTCCAGCACTTCTCTGTGTTTTACAGACCTTTTTTATAAATAAAATGTTTCATCA  
GCTGCATAAAAAAAAAAAAAA

**FIGURE 330**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAE EEGQETMKGRVSIRD SRQELSLIVTLWNLTLQDAGEYWCGVEKRGPD E SLLISLFV  
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAE E KEAPSQAPEGD  
VISMPPLHTSEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128